STIC-Biotech/ChemLib 79094

From: Portner, Ginny
Sent: Wednesday, October 30, 2002 3:18 PM
To: STIC-Biotech/ChemLib
Subject: priority search

Importance: High

① ②

Please search the sequences in Application 09/910,186 against 08/123,975; 60146,192; 60/133,866; 60/133868; 60/133869; 60/133,865; 60133,873 and 60/133,867. Thanks

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Ginny,
None of the provisional cases have CRF's, so I could only compare ① with ②.
Barb

RECEIVED
OCT 30 2002
(STIC)

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BOB
Phone:
Location:
Date Picked Up: 11-7
Date Completed: 11-7-02
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other: 1

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-1.res made by bobryen on Thu 7 Nov 102 14:39:29-PST.


Query sequence being compared:US-09-910-186A-1 (1-1332)
Number of sequences searched:                         3
Number of scores above cutoff:                        3

      Results of the initial comparison of US-09-910-186A-1 (1-1332) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                         *
S    0----------------------------------------------------------------------
      |      |      |    | |      |      |     ||      |      |       |
SCORE 0    146    291    437    583    728    874    1020   1165   1311
STDEV                   -1                     0


                              PARAMETERS

Similarity matrix       Unitary    K-tuple                     4
Mismatch penalty              1    Joining penalty            30
Gap penalty                5.00    Window size               500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                           SEARCH STATISTICS

Scores:                 Mean      Median     Standard Deviation
                        1053      539         446.29

Times:                  CPU                  Total Elapsed
                   00:00:00.00               00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                             Init.  Opt.
Sequence Name     Description                         Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338  1311  1314   0.58   0
   2. US-08-123-975A-1 Sequence 1, Application U   1338  1311  1314   0.58   0
                 ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351   538   704  -1.15   0


1. US-09-910-186A-1 (1-1332)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =   1311  Optimized Score  =   1314  Significance =  0.58
Residue Identity  =    98%  Matches          =   1318  Mismatches   =    13
Gaps              =      5  Conservative Substitutions              =     0

    X      10        20        30        40        50        60        70
   GAATTCGAAACGATGCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTG
         |  | |   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTG
    X       10        20        30        40        50        60        70

         80        90       100       110       120       130       140
   AACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAA
          80        90       100       110       120       130       140

      150       160       170       180       190       200       210
   GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
       150       160       170       180       190       200       210

    220       230       240       250       260       270       280
   CTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAA
     220       230       240       250       260       270       280

  290       300       310       320       330       340       350       360
   TACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAA
   290       300       310       320       330       340       350

          370       380       390       400       410       420       430
   GTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
 360       370       380       390       400       410       420       430

        440       450       460       470       480       490       500
   AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
         440       450       460       470       480       490       500

      510       520       530       540       550       560       570
   CTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
       510       520       530       540       550       560       570

    580       590       600       610       620       630       640
   CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATAC
     580       590       600       610       620       630       640

  650       660       670       680       690       700       710       720
   TTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGT
   650       660       670       680       690       700       710

         730       740       750       760       770       780       790
   ATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCG
 720       730       740       750       760       770       780       790

        800       810       820       830       840       850       860
   AACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTT
         800       810       820       830       840       850       860

      870       880       890       900       910       920       930
   ATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCT
       870       880       890       900       910       920       930

    940       950       960       970       980       990      1000
   GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATAC
     940       950       960       970       980       990      1000

 1010      1020      1030      1040      1050      1060      1070      1080
   CGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGT
  1010      1020      1030      1040      1050      1060      1070

         1090      1100      1110      1120      1130      1140      1150
   AATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTG
1080      1090      1100      1110      1120      1130      1140      1150

       1160      1170      1180      1190      1200      1210      1220
   CAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCT
        1160      1170      1180      1190      1200      1210      1220

     1230      1240      1250      1260      1270      1280      1290
   TCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTT
      1230      1240      1250      1260      1270      1280      1290

   1300      1310      1320          1330 X
   GATGACGGTTGGGGTGAACGTCCGCTGTAA-----GAATTC
   ||||||||||||||||||||||||||||||     |||  |
   GATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
    1300      1310      1320      1330    X


2. US-09-910-186A-1 (1-1332)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    1311  Optimized Score  =    1314  Significance =  0.58
Residue Identity  =     98%  Matches          =    1318  Mismatches   =    13
Gaps              =       5  Conservative Substitutions              =     0

    X      10        20        30        40        50        60        70
   GAATTCGAAACGATGCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTG
         |  | |   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTG
    X       10        20        30        40        50        60        70

         80        90       100       110       120       130       140
   AACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAA
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   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAA
          80        90       100       110       120       130       140

      150       160       170       180       190       200       210
   GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC
       150       160       170       180       190       200       210

    220       230       240       250       260       270       280
   CTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAA
     220       230       240       250       260       270       280

  290       300       310       320       330       340       350       360
   TACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAA
   290       300       310       320       330       340       350

          370       380       390       400       410       420       430
   GTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
 360       370       380       390       400       410       420       430

        440       450       460       470       480       490       500
   AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
         440       450       460       470       480       490       500

      510       520       530       540       550       560       570
   CTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
       510       520       530       540       550       560       570

    580       590       600       610       620       630       640
   CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATAC
     580       590       600       610       620       630       640

  650       660       670       680       690       700       710       720
   TTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGT
   650       660       670       680       690       700       710

         730       740       750       760       770       780       790
   ATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCG
 720       730       740       750       760       770       780       790

        800       810       820       830       840       850       860
   AACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTT
         800       810       820       830       840       850       860

      870       880       890       900       910       920       930
   ATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCT
       870       880       890       900       910       920       930

    940       950       960       970       980       990      1000
   GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATAC
      940       950       960       970       980       990      1000

  1010      1020      1030      1040      1050      1060      1070      1080
    CGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGT
   1010      1020      1030      1040      1050      1060      1070

          1090      1100      1110      1120      1130      1140      1150
    AATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTG
 1080      1090      1100      1110      1120      1130      1140      1150

        1160      1170      1180      1190      1200      1210      1220
    CAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCT
         1160      1170      1180      1190      1200      1210      1220

      1230      1240      1250      1260      1270      1280      1290
    TCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTT
       1230      1240      1250      1260      1270      1280      1290

    1300      1310      1320           1330 X
    GATGACGGTTGGGGTGAACGTCCGCTGTAA-----GAATTC
    ||||||||||||||||||||||||||||||     |||  |
    GATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
     1300      1310      1320      1330     X


3. US-09-910-186A-1 (1-1332)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    538  Optimized Score =    704  Significance = -1.15
Residue Identity  =    55%  Matches         =    759  Mismatches   =   530
Gaps              =     71  Conservative Substitutions              =     0

        10        20    X   30        40        50        60        70
    TCGAAACGATGCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACC
                            | ||||   ||||||      | ||| | || |    |||||||||||
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X       10        20        30        40        50

      80        90       100       110       120       130       140
    TGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTA
    |||| ||| ||  |||  | |||||||| |||||| | |||| | | ||| |  |  |   | | |  ||
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT--ATACGACGGT--
          60        70        80        90       100       110         120

   150       160       170       180       190       200       210       220
    ACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGA
       | || | ||  |||||||| ||| || | |||  |  |   |     || || |||   ||||  | ||
    --GTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGA
             130       140       150       160       170       180       190

           230       240       250       260       270       280       290
    AGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACT
    |  |    ||| | | ||||||  | | |    |||||||    |||||||||||||||||||||||||||
    ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
           200       210       220       230       240       250       260

         300                310       320       330       340       350
    TCAACTCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTT
      |||  |         |  |   |  ||||||||||||||||||||||||||||| | || || |||||||
    AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTT
         270       280       290       300       310       320       330

      360       370       380       390       400       410       420
    GGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTG
    ||||  | ||  |   |         |||||||||||||||   || |   | |  |  |   |   |||
    GGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTAT
       340       350       360       370       380       390       400

    430       440       450       460       470       480       490
    TATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACA
    | ||| |||||             |||||||||| ||||||||||||||| ||||||||||||||||||| |
    TCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATA
     410       420       430       440       450       460       470

  500       510       520       530       540       550       560       570
    ATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTA
    |    ||||| ||  | |||||||||||||||||    |||       | |     |||    |  |  ||
    A---CCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTG
      480       490       500       510       520       530       540

          580       590       600       610       620       630       640
    ACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCA
    |  |   ||||     | | ||||| |||||||||||||||      ||   |  ||  | ||||||||| |
    AAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGA
    550       560       570       580       590       600       610

        650       660       670       680       690       700       710
    AATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATT
    ||||||||    | ||| |||  ||||||    |     | ||| |||| | |||| | | ||||||  | |
    AATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACT
  620       630       640       650       660       670       680       690

      720       730       740       750       760       770       780
    CTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACG
    | |    ||||||||||||||||||| |    |||  |||| |||||   ||||| ||| | |||
    CCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTA
          700       710       720       730       740       750       760

    790       800       810       820       830       840       850
    ATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTT
    |   ||||   ||| |  |  | || || |    |      ||| | ||   |||||   || |
    ACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAAT---CCTGACTCGTTCCAAATACA
        770       780       790       800       810          820       830

  860       870       880       890       900       910       920
    CTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT------CAAGA
         |   |||   ||||| ||    ||     |||||||   |||   || ||||||||      |||
    ACCAGAACTCTAAATACATCAAC---TACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAAT
         840       850          860       870       880       890       900

      930       940       950       960       970       980       990
    AATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGA
       || |       | ||| ||  | ||||| || ||  | ||     | ||| |  |  |  |      ||
    CTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGA
          910       920       930       940       950       960       970

   1000      1010          1020      1030      1040      1050      1060
    ACAAAGAATACCGTCT----GGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAA
    |  | ||||  ||| |      |||| | | ||||  ||   |  | ||||||| | ||    |||| |
    ATCAGGAATGGCGTGTATACACCTACAAGTACTTC-AAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCG---
        980       990      1000       1010      1020      1030      1040

     1070      1080      1090      1100      1110      1120         1130
    ATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTA---TCACTAAC
    ||| | ||    |   | || |   |     |    || |||    |  |||| |||   |    | ||  |
    ATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGC
         1050      1060      1070      1080      1090      1100      1110

      1140      1150      1160      1170      1180      1190      1200
    AAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAA-
     |        | ||     | ||  |   |  | |||| |||||| | |||||| ||||||  ||| || |
    CAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAA
       1120      1130      1140      1150      1160      1170      1180

          1210                1220              1230            1240
    -----TATCG----------CTAAACTGGTTGCT--------TCCAACTGGTAC------AATCGTCAGATC
         |||||           || |  |  | ||        ||||| ||||||       |   | |   |
  TCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGC
   1190      1200      1210      1220      1230      1240      1250

1250      1260      1270      1280      1290      1300      1310      1320
  GAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCG
   |||  | |   |  |  |||||||||  |||| |||||||||||   || || ||||||   |||
  AAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAA
 1260      1270      1280      1290      1300      1310      1320

        1330 X
  CTGTAAGAATTC
  |    ||| |
  CCTCTAGAGTCGAGGCCTGCAG
1330      1340      1350
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-1-inv.res made by bobryen on Thu 7 Nov 102 14:39:50-PST.


Query sequence being compared:US-09-910-186A-1' (1-1332)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-1' (1-1332) with:
        File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                  *
N     -
C     -
E     -                                                              *
S    0----------------------------------------------------------------------
      |     ||      |      |      |      | |    | |    | |    |  |   |
SCORE 0     |6     12     18     24     31 |   37 |   43 |   49  |  55
STDEV      -6      -5     -4     -3       -2     -1      0       1


                              PARAMETERS

Similarity matrix       Unitary      K-tuple                  4
Mismatch penalty              1      Joining penalty         30
Gap penalty                5.00      Window size            500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                              SEARCH STATISTICS

Scores:                 Mean       Median       Standard Deviation
                         47          45               6.35

Times:                  CPU                     Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                     4027
Number of sequences searched:              3
Number of scores above cutoff:             3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name      Description                     Length Score Score  Sig. Frame
---------------------------------------------------------------------------------
                       ****  1 standard deviation above mean ****
   1. US-08-123-975A-6 Sequence 6, Application U    1351    55   432   1.26   0
                       ****  0 standard deviation from mean ****
   2. US-08-123-975A-4 Sequence 4, Application U    1338    44   479  -0.47   0
   3. US-08-123-975A-1 Sequence 1, Application U    1338    44   479  -0.47   0


1. US-09-910-186A-1' (1-1332)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    55  Optimized Score   =   432  Significance =  1.26
Residue Identity  =   40%  Matches           =   515  Mismatches   =   658
Gaps              =    87  Conservative Substitutions              =     0

   80        90       100       110       120       130       140       150
    CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAAACCGATG
                           | |   | |||  |   |  ||| ||  |  |     |        |
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X       10        20        30        40        50

          160       170       180       190       200       210       220
    AAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTCGTTCTTG
          | |  |  | || | |  ||   | |  |  ||  |    |     |||       | || | |||
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90       100       110       120

        230       240       250       260       270       280       290
    GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTTTTCTACA
     | |  || ||||  ||| |   || | |  |  | ||||  |  ||          ||||||  |  |||
    AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGTGTTAC-
       130       140        150       160       170                180

      300       310       320       330       340       350       360
    CCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATACACGATCA
     |||  | ||||  |||      | |  | |||||| | |         ||  |  || |   | |  ||||
    TCAGAATCAGAA-CATCATCTTCAACTCCGTATTCCTGG---------ACTTCTCTGTTTCCTTCTGGATCC
      190        200       210       220                230       240

    370       380       390        400       410       420       430
    TTGTTGCGAACGATATTGTCCTTGTTA-CCAGACGCGTATTTCTTGATGATGAATTTGGTACCACGGTACAG
     | |  ||||  | |    |   | || |||||     ||         ||  |       | || | |
    GTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGA
    250       260       270       280       290       300       310

   440       450           460        470       480       490       500
    GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCACGCGGACCTTTCAGGTACATGTAACCG
     ||| |  || |||    |||| |   |  |   |||| | | ||   ||||   || | |  || | | ||
    AGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGAC---TCTGATCGATATCAACG
  320       330       340       350       360       370          380

      510       520       530       540       550       560       570
    CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGTACGGTTTGTCG
       | ||| |   |||   | || |  ||     || |     |||   ||      ||   |  |   | |
    GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCGCTGG
   390       400       410        420       430          440       450

    580       590       600       610       620       630       640
    TACTGCAGGTAGTCACCCCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCTTTGATT
    | || |  ||   || | |  |   | |  |  || | | |||     |    |    || ||  | | ||
    TTCTTC--GTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATA
     460         470       480       490       500       510       520

  650       660             670       680          690       700       710
    TCTTTTTCGTTCAGTTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCGGTGAGTG
     |    ||    |  ||       || |||   |   ||||    | ||  | |  || |  |   |   |
    CCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATC
     530       540       550       560       570       580       590

         720       730       740       750       760            770
    TCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG------ATTGGAGATC
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     ||      | ||  | |  || |       ||    | |   ||  |  | |||      || | ||| |
   GTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAAC
  600       610       620       630       640       650       660       670

  780       790       800          810       820       830       840
   GGTTTCTGGTCGATCAGACGGCCGTTGATGT---AGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTA
   |||    | || |        |||   |  |   ||| ||  | | || || |  |||        |    |
   GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGAT------GTACAACA
          680       690       700       710       720             730

   850       860       870       880       890       900       910
   ACGAAGATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTTTG
   | ||| |      | |  |||  |  |   |      | |  | | | |     || ||    || |   ||
   AAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTG
    740       750       760       770       780       790       800

 920       930       940       950       960       970       980       990
   ATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGTTT
   |  ||||||   || | |  | | ||          | | | |  | | | |    | | |  ||  |||
   AAATCCTGA--CTCGTTCCAAATACA--------ACCAGAACTCTAAATACATCAACTACCGCGACCTGTAC
  810         820       830               840       850       860       870

        1000      1010      1020      1030      1040      1050      1060
   TCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTATTTCGGGATACGGATCCAG
     |    |   | | ||  |   |      |  |       |    | ||  ||  |    |||| |   |
   ATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAA
          880       890       900       910       920       930       940

      1070         1080      1090      1100      1110      1120      1130
   AAGGAGGTGGA---GAAGTTTTCGTACATAGAGTTGTATACGATAGCATTCTTCAGGATAACTTCGATTTTG
    |  |  |  |   | | || |   || |  |   | |   |   | || |  |   |     |  |
   GACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAA
        950       960       970       980       990      1000      1010

       1140      1150      1160      1170      1180      1190      1200
   GAAGATTCCAGATTGAACAGCTGGATCTGATTCTTGTCGATCGGATCGAAGTTAACTTTAGAACCGATGTTG
   |||||         ||| ||||    |||  ||   ||  || |||       |||| || |||  |   |
   GAAGA--------AGAAAAGCTTTTCCTGGCTCCGATC--TCTGATTCCGACGAACTCTACAAC--ACCATC
             1020      1030      1040        1050      1060        1070

     1210      1220      1230      1240      1250      1260      1270
   ATTTTGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGTTCAGGATGGAGGTATTG
       |  |||  ||    ||   | ||| |   |  |   |   |  |  || |   | |||| ||    |
   CAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAG--AAAGATGAAGAATCTA
     1080      1090      1100      1110      1120        1130      1140

   1280      1290      1300      1310      1320      1330 X
   ATGATGTTCTTGATGTATTCAGTGAAGGTAGACAGCAGACGCATCGTTTCGAATTC
    ||| |   | | | |  || ||       |     |      | || ||| ||||
   CTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACT
     1150      1160      1170      1180      1190      1200      1210

   ACTT
   1220


2. US-09-910-186A-1’ (1-1332)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     44  Optimized Score  =    479  Significance = -0.47
Residue Identity =    43%  Matches          =    584  Mismatches   =   689
Gaps             =     85  Conservative Substitutions          =     0

           10        20        30        40        50        60        70
   GAATTCTTACAGCGGACGTTCACCCCAACCGTCATCAACCGGGATGAACTCCCAAGAGCAACCCAGAGTGCG
                      ||   |||    || ||   | |  |    || |   |   | | |||
                     CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
                     X       10         20        30        40        50

         80        90       100       110       120       130       140
   AGAGGAACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
   |     || | |   ||||       ||| |    | | | ||| |     |||     ||    | |  |
   ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
        60        70               80        90       100       110

      150       160       170       180       190       200       210
   ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
    |     ||| | | |||| | | |  |||  | |   ||| |  |   ||    | ||    |  ||| ||
   GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGAATCAGATCCA-GCTGTTC
    120       130       140       150         160       170        180

    220       230       240       250       260       270       280
   GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
     ||| | || |    | | | |  | |  |   | |  || |     |  | | |    |   | ||
   AATCTGGAATCTTCCAAAATCGAAGTTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAAC
     190       200       210          220       230       240       250

  290       300       310       320       330       340       350       360
   TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
   |||| ||||  | |     | ||  ||| ||   ||  || |||       | ||     |   ||| ||||
   TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
      260          270       280          290       300       310       320

              370       380       390       400        410       420
   ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
   || |||||    ||    |||    ||| |  |||  |     | | | | | |      || |  | |
   ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
          330       340       350       360       370       380       390

   430       440       450       460         470       480       490
   CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
   |  | | |||   | ||  |||   ||    | ||| ||  |||     |        || | || |  |||
   CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
        400       410       420       430       440       450       460

    500       510       520       530       540         550       560
   ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
   ||  | |   ||||     | | |||  | ||| |     |  || ||     | || | ||  |||  |
   ATCAATCGCTGGAT-----CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACG
      470            480       490       500       510       520       530

    570        580       590          600       610       620       630
   ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
    | || || |||  | | |     || ||   |  |    | | || | | | |  |      || |
   GCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAAC
         540       550       560       570       580       590       600

      640       650       660       670       680       690       700
   TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
   |  | |  | |  |  |  |  |    |  |||   || || |  |  |  | || ||   |||  |    |
   TGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACG
       610       620       630       640       650       660       670

    710       720       730       740       750       760       770
   TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
     |  |  |  | |  | |  |     | ||      |  |   | | || | |    |  |   || ||
   AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
     680       690       700       710       720       730          740

  780       790       800       810       820       830       840       850
   GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTAACG
      | | |  ||| || || |   |  |||  || | || |     || ||  |     | ||| |  |||
   ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
      750        760       770       780         790       800       810

               860       870       880       890       900       910
   AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
   | |     ||||   | |  |||||  |    | | |   | |      || | ||| ||| |    ||
   ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
       820       830         840       850       860        870       880

   920       930       940       950       960       970       980
   TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
   |||  || |   ||| | |  |   ||| ||   |   |   |  |  | |     |  |||  | |||
   TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
        890       900        910       920       930       940       950
   990      1000      1010      1020      1030      1040         1050
     TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
      |||    ||    ||||| |||||| |||   |     || |       ||| ||    || || |||
     GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
         960           970       980       990      1000      1010      1020

      1060      1070      1080      1090      1100         1110      1120
     GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
      | | |  | |  |||| ||||    || |   |    | | |  |   |       |  || |  | |  |
     TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
          1030      1040      1050      1060      1070      1080      1090

       1130      1140      1150       1160      1170        1180      1190
     CGATTTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
      | | |    | || | |||  || || | |    || |    ||   |  | |||   | |  |||  | |
     AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
          1100      1110      1120      1130      1140      1150      1160

        1200        1210      1220      1230      1240      1250
     AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGT----
      | |||| | | |||  | |      | |    ||     |||     | ||| | | |    | |||
     TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAA
        1170      1180      1190      1200      1210      1220      1230

     1260      1270      1280          1290      1300      1310      1320
     ---TCAGGATGGAGGTATTGATGATGTTC----TTGATGTATTCAGTGAAGGTAGACAGCAGACGCATCGTT
        ||||   | | ||     |     ||    ||| | |    |||  |    |   |  ||||  | |
     TCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGG
      1240      1250      1260      1270      1280      1290      1300

       1330 X
     TCGAATTC
     |  |  ||
     TGAACGTCCGCTGTAACCCGGGAAAGCT
    1310      1320      1330


3. US-09-910-186A-1' (1-1332)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =     44  Optimized Score =     479  Significance = -0.47
Residue Identity  =    43%  Matches         =     584  Mismatches   =   689
Gaps              =     85  Conservative Substitutions     =            0

             10        20        30        40        50        60        70
     GAATTCTTACAGCGGACGTTCACCCCAACCGTCATCAACCGGGATGAACTCCCAAGAGCAACCCAGAGTGCG
                        ||   |||    || ||   | |  |    || |   |   | | |||
                       CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
                       X       10          20        30        40        50

           80        90       100       110       120       130       140
     AGAGGAACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
     |     || | |   ||||       ||| |    | | | ||| |     |||     ||    | |  |
     ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
          60        70               80        90       100       110

        150       160       170       180       190       200       210
     ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
      |     ||| | | |||| | | |  |||  | |   ||| |  |   ||    | ||    |  ||| ||
     GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGAATCAGATCCA-GCTGTTC
      120       130       140       150         160       170        180

      220       230       240       250       260       270       280
     GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
       ||| | || |    | | | |  | |  |   | |  || |     |  | | |    |   | ||
     AATCTGGAATCTTCCAAAATCGAAGTTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAAC
       190       200       210          220       230       240       250

    290       300       310       320       330       340       350       360
     TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
     |||| ||||  | |     | ||  ||| ||   ||  || |||       | ||     |   ||| ||||
     TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
        260          270       280          290       300       310       320

                370       380       390       400        410       420
     ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
     || |||||    ||    |||    ||| |  |||  |     | | | | | |      || |  | |
     ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
            330       340       350       360       370       380       390

     430       440       450       460         470       480       490
     CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
     |  | | |||   | ||  |||   ||    | ||| ||  |||     |        || | || |  |||
     CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
          400       410       420       430       440       450       460

      500       510       520       530       540         550       560
     ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
     ||  | |   ||||     | | |||  | ||| |     |  || ||     | || | ||  |||  |
     ATCAATCGCTGGAT-----CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACG
        470            480       490       500       510       520       530

      570        580       590          600       610       620       630
     ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
      | || || |||  | | |     || ||   |  |    | | || | | | |  |      || |
     GCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAAC
           540       550       560       570       580       590       600

        640       650       660       670       680       690       700
     TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
     |  | |  | |  |  |  |  |    |  |||   || || |  |  |  | || ||   |||  |    |
     TGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACG
         610       620       630       640       650       660       670

      710       720       730       740       750       760       770
     TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
       |  |  |  | |  | |  |     | ||      |  | | | | || | |    |  |   || ||
     AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
       680       690       700       710       720       730        740

    780       790       800       810       820       830       840       850
     GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTAACG
        | | |  ||| || || |   |  |||  || | || |     || ||  |     | ||| |  |||
     ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
        750        760       770       780         790       800       810

                 860       870       880       890       900       910
     AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
     | |     ||||   | |  |||||  |    | | |   | |      || | ||| ||| |    ||
     ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
         820       830         840       850       860        870       880

     920       930       940       950       960       970       980
     TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
     |||  || |   ||| | |  |   ||| ||   |   |   |  |  | |     |  |||  | |||
     TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
          890       900        910       920       930       940       950

   990      1000      1010      1020      1030      1040         1050
     TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
      |||    ||    ||||| |||||| |||   |     || |       ||| ||    || || |||
     GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
         960           970       980       990      1000      1010      1020

      1060      1070      1080      1090      1100         1110      1120
     GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
      | | |  | |  |||| ||||    || |   |    | | |  |   |       |  || |  | |  |
     TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
          1030      1040      1050      1060      1070      1080      1090

       1130      1140      1150       1160      1170        1180      1190
     CGATTTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
      | | |    | || | |||  || || | |    || |    ||   |  | |||   | |  |||  | |
     AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
          1100      1110      1120      1130      1140      1150      1160
      1200        1210      1220      1230      1240      1250
   AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGT----
    | |||| | | |||  | |      | |    ||     |||     | ||| | | |    | |||
   TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAA
    1170      1180      1190      1200      1210      1220      1230

   1260      1270      1280          1290      1300      1310      1320
   ---TCAGGATGGAGGTATTGATGATGTTC----TTGATGTATTCAGTGAAGGTAGACAGCAGACGCATCGTT
      ||||   | | ||     |     ||    ||| | |    |||  |    |   |  ||||  | |
   TCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGG
  1240      1250      1260      1270      1280      1290      1300

     1330 X
   TCGAATTC
   |  |  ||
   TGAACGTCCGCTGTAACCCGGGAAAGCT
1310      1320      1330
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-2.res made by bobryen on Thu 7 Nov 102 14:31:34-PST.


Query sequence being compared:US-09-910-186A-2 (1-437)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-2 (1-437) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -                           * *                                 *
S    0----------------------------------------------------------------------
      |      |  |   |      |      |   |   |      |      | |    |      |
SCORE 0     46  |  92    138    184   | 231    277    323 |  369    415
STDEV          -1                     0                   1

                          PARAMETERS

Similarity matrix       PAM-150     K-tuple                  1
Threshold level of sim.    16%
Mismatch penalty             1      Joining penalty         20
Gap penalty               5.00      Window size            437
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0
                         SEARCH STATISTICS

Scores:                  Mean        Median       Standard Deviation
                          262          181         132.08

Times:                    CPU                     Total Elapsed
                     00:00:00.00                  00:00:00.00

Number of residues:                 1704
Number of sequences searched:          3
Number of scores above cutoff:         3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                             Init. Opt.
Sequence Name     Description                         Length Score Score  Sig. Frame
-----------------------------------------------------------------------------------
                        ****  1 standard deviation above mean ****
   1. US-08-123-975A-3 Sequence 3, Application U     415    415    415    1.16    0
                        ****  0 standard deviation from mean ****
   2. US-08-123-975A-5 Sequence 5, Application U     439    193    273   -0.52    0
   3. US-08-123-975A-2 Sequence 2, Application U     850    180    276   -0.62    0


1. US-09-910-186A-2 (1-437)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     415  Optimized Score  =    415  Significance =  1.16
Residue Identity =     100%  Matches          =    415  Mismatches    =     0
Gaps              =       0  Conservative Substitutions              =     0

          10        20  X     30        40        50        60        70
    LLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                        ||||||||||||||||||||||||||||||||||||||||||||||||||||
                        RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                        X        10        20        30        40        50

        80        90       100       110       120       130       140
    YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
          60        70        80        90       100       110       120

     150       160       170       180       190       200       210
    NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
       130       140       150       160       170       180       190

   220       230       240       250       260       270       280       290
    ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
     200       210       220       230       240       250       260

           300       310       320       330       340       350       360
    LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
   270       280       290       300       310       320       330       340

         370       380       390       400       410       420       430
    VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
           350       360       370       380       390       400       410


     X
    RPL
    |||
    RPL
     X


2. US-09-910-186A-2 (1-437)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =     193  Optimized Score  =    273  Significance = -0.52
Residue Identity =      38%  Matches          =    169  Mismatches    =   230
Gaps              =      17  Conservative Substitutions              =    26

          X 10        20        30        40        50        60        70
    MRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNA
          |  |   | |  ||||||  | ||||| |::|: :   |     ||||  |     ||| |
          FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQN
          X        10        20        30        40          50        60
          80        90          100       110       120       130       140
    IVYNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFK
    |::|| :  || ||||||||| |        ||||||||| ||||||:|     ||||| |       | |
    IIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFE
        70        80        90       100       110       120       130

          150       160       170       180       190       200       210
    YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYF
    |     ||:||||| ||||||| |||:||||||:|     |     : |   | |||||  |   :|| |||
    YNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYF
     140       150        160       170       180       190       200

        220       230       240       250       260       270       280
    NLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVM
      |  ||    | : |  || |  ||||||  | | | ||| |    | |:        |    :
    SIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNS
    210       220       230       240       250       260       270

      290       300       310       320       330       340       350
    TTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGN
        |             |  :    | |||  | :|      | | |  |       |  |    | |
    KYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDE
  280       290       300       310       320       330       340       350

    360       370        380       390       400                 410
    LSQVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA--------SNWYNRQIERS--SRT
        :  |   :|            :    :|| || | |   :            | || : : |
    FYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLK
          360       370       380       390       400       410       420

   420       430   X
    LGCSWEFIPVDDGWGERPL
    ||| | ||| |:|| |
    LGCNWQFIPKDEGWTE
        430        X

3. US-09-910-186A-2 (1-437)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    180  Optimized Score  =    276  Significance  = -0.62
Residue Identity =    37%  Matches          =    170  Mismatches    =   235
Gaps             =     17  Conservative Substitutions               =    26

                        X       10        20        30        40        50
                        MRLLSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDK
                          |   |  |   | |  ||||||  | ||||| |::|: :   |     ||
    KVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DK
      390       400     X 410       420       430       440       450

          60        70        80        90           100       110       120
    NQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNY
    ||  |     ||| |     |::|| :  || ||||||||| |        ||||||||| ||||||:|
    NQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRG
      460       470       480       490       500       510       520

          130       140       150       160       170       180       190
    GEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNN
      ||||| |       | | |     ||:||||| ||||||| |||:||||||:|     |     : |
    NRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGE
    530       540       550       560        570       580       590

        200       210       220       230       240       250       260
    IMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVD
    | |||||  |   :|| |||  |  ||    | : |  || |  ||||||  | | | ||| |    | |:
    IIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIK
   600       610       620       630       640       650       660       670

      270       280       290       300       310       320       330
    VNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATN
           |    :           |             |  :    | |||  | :|      | | |  |
    LKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTY

           680       690       700       710       720       730       740

    340       350       360       370        380       390       400
    ASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA----
          |  |    | |       :  |   :|            :    :|| || | |   :
    KYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKD
         750       760       770       780       790       800       810

           410         420       430   X
    ----SNWYNRQIERS--SRTLGCSWEFIPVDDGWGERPL
        | || : : |      ||| | ||| |:|| |
    YFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
       820       830       840       850
```

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> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3.res made by bobryen on Thu 7 Nov 102 14:40:15-PST.

Query sequence being compared:US-09-910-186A-3 (1-1323)
Number of sequences searched:                         3
Number of scores above cutoff:                        3

      Results of the initial comparison of US-09-910-186A-3 (1-1323) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                           *
N     -
C     -
E     -                        *
S    0------------------------------------------------------------------
      |      |      |   | |      |      |    ||      |      |     |
SCORE 0    145    290   435    580    724   869   1014   1159  1304
STDEV                  -1                    0

                              PARAMETERS

Similarity matrix       Unitary      K-tuple                    4
Mismatch penalty              1      Joining penalty           30
Gap penalty                5.00      Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                              SEARCH STATISTICS

Scores:                 Mean         Median      Standard Deviation
                        1048          539         442.25

Times:                  CPU                      Total Elapsed
                   00:00:00.00                   00:00:00.00

Number of residues:                     4027
Number of sequences searched:              3
Number of scores above cutoff:             3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338  1304  1305   0.58   0
   2. US-08-123-975A-1 Sequence 1, Application U   1338  1304  1305   0.58   0
                **** 1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351   538   704  -1.15   0

1. US-09-910-186A-3 (1-1323)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =   1304  Optimized Score  =   1305  Significance =  0.58
Residue Identity =     98%  Matches          =   1309  Mismatches   =    14
Gaps              =      5  Conservative Substitutions              =     0

         X      10        20        30        40        50        60
         GAATTCGAAACGATGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
                    | |||||||||||||||||||||||||||||||||||||||||||||||||||
 CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
         10        20        30        40        50        60        70

     70        80        90       100       110       120       130
 ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
       80        90       100       110       120       130       140

  140       150       160       170       180       190       200
 TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
  150       160       170       180       190       200       210

210       220       230       240       250       260       270       280
 TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
 220       230       240       250       260       270       280

        290       300       310       320       330       340       350
 ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
290       300       310       320       330       340       350       360

      360       370       380       390       400       410       420
 TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
        370       380       390       400       410       420       430

    430       440       450       460       470       480       490
 AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
      440       450       460       470       480       490       500

  500       510       520       530       540       550       560
 TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
    510       520       530       540       550       560       570

570       580       590       600       610       620       630       640
 ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
  580       590       600       610       620       630       640

        650       660       670       680       690       700       710
 TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
 650       660       670       680       690       700       710       720

       720       730       740       750       760       770       780
  TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
         730       740       750       760       770       780       790

     790       800       810       820       830       840       850
  ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
       800       810       820       830       840       850       860

   860       870       880       890       900       910       920
  TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
     870       880       890       900       910       920       930

 930       940       950       960       970       980       990      1000
  GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
   940       950       960       970       980       990      1000

        1010      1020      1030      1040      1050      1060      1070
  GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
1010      1020      1030      1040      1050      1060      1070      1080

      1080      1090      1100      1110      1120      1130      1140
  ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
        1090      1100      1110      1120      1130      1140      1150

    1150      1160      1170      1180      1190      1200      1210
  AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
      1160      1170      1180      1190      1200      1210      1220

  1220      1230      1240      1250      1260      1270      1280
  CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
    1230      1240      1250      1260      1270      1280      1290

1290      1300      1310           1320  X
  ATGACGGTTGGGGTGAACGTCCGCTGTAA-----GAATTC
  |||||||||||||||||||||||||||||     |||  |
  ATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
  1300      1310      1320      1330     X


2. US-09-910-186A-3 (1-1323)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =   1304  Optimized Score  =   1305  Significance =  0.58
Residue Identity =    98%  Matches          =   1309  Mismatches   =    14
Gaps             =      5  Conservative Substitutions             =     0

          X        10        20        30        40        50        60
          GAATTCGAAACGATGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
                     | |||||||||||||||||||||||||||||||||||||||||||||||||||
  CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
          10        20        30        40        50        60        70

      70        80        90       100       110       120       130
  ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
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  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
        80        90       100       110       120       130       140

   140       150       160       170       180       190       200
  TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
     150       160       170       180       190       200       210

 210       220       230       240       250       260       270       280
  TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
   220       230       240       250       260       270       280

         290       300       310       320       330       340       350
  ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
 290       300       310       320       330       340       350       360

       360       370       380       390       400       410       420
  TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
         370       380       390       400       410       420       430

     430       440       450       460       470       480       490
  AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
       440       450       460       470       480       490       500

   500       510       520       530       540       550       560
  TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
     510       520       530       540       550       560       570

 570       580       590       600       610       620       630       640
  ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
   580       590       600       610       620       630       640

         650       660       670       680       690       700       710
  TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
 650       660       670       680       690       700       710       720

       720       730       740       750       760       770       780
  TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
         730       740       750       760       770       780       790

     790       800       810       820       830       840       850
  ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
       800       810       820       830       840       850       860

   860       870       880       890       900       910       920
  TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
     870       880       890       900       910       920       930

 930       940       950       960       970       980       990      1000
  GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
    940       950       960       970       980       990      1000

         1010      1020      1030      1040      1050      1060      1070
   GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
 1010      1020      1030      1040      1050      1060      1070      1080

       1080      1090      1100      1110      1120      1130      1140
   ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
         1090      1100      1110      1120      1130      1140      1150

     1150      1160      1170      1180      1190      1200      1210
   AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
       1160      1170      1180      1190      1200      1210      1220

   1220      1230      1240      1250      1260      1270      1280
   CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
     1230      1240      1250      1260      1270      1280      1290

 1290      1300      1310           1320  X
   ATGACGGTTGGGGTGAACGTCCGCTGTAA-----GAATTC
   |||||||||||||||||||||||||||||     |||  |
   ATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGAAAGCTT
   1300      1310      1320      1330     X


3. US-09-910-186A-3 (1-1323)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    538  Optimized Score  =    704  Significance = -1.15
Residue Identity =    55%  Matches          =    763  Mismatches   =   526
Gaps             =     74  Conservative Substitutions              =     0

           10  X     20        30        40        50        60        70
   GAATTCGAAACGATGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGC
               ||| ||   ||||   ||||||      | ||| | || |    |||||||||||||||
               ATGGCT---TTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGT
               X          10        20        30        40        50

         80        90       100       110       120       130       140
   TACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTC
   ||| ||  |||  | |||||||| |||||| | |||| | | ||| |  |  |   | | |  ||     |
   TACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT--ATACGACGGT----GTT
    60        70        80        90       100       110         120

      150       160       170       180       190       200       210
   GATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAAT
   || | ||  |||||||| ||| || | |||  |  |   |     || || |||   ||||  | |||  |
   GAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAG
       130       140       150       160       170       180       190

    220       230       240       250       260       270       280
   GCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAAC
      ||| | | ||||||  | | |    |||||||    |||||||||||||||||||||||||||   |||
   AACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAAC
     200       210       220       230       240       250       260

  290                300       310       320       330       340       350
   TCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAA
     |         |  |   |  |||||||||||||||||||||||||||| | || || |||||||||||
   GACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAG
   270       280       290       300       310       320       330

         360       370       380       390       400       410       420
   GTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTC
    | ||  |   |         |||||||||||||||   || |   | |  |  |   |   |||  | |||
   ATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTC
 340       350       360       370       380       390       400       410

       430       440       450       460       470       480       490
   AAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGT
    |||||             |||||||||| ||||||||||||||| ||||||||||||||||||  ||
   GAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAA---C
         420       430       440       450       460       470          480

     500       510       520       530       540       550       560
   CTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATC
   ||||| ||  | |||||||||||||||||    |||       | |     |||    |  |  || |  |
   CTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTT
          490       500       510       520       530       540       550

   570       580       590       600       610       620       630
   CACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATAC
     ||||     | | ||||| |||||||||||||||      ||   |  ||  | ||||||||| ||||||
   ATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATAC
        560       570       580       590       600       610       620

 640       650       660       670       680       690       700       710
   TTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGT
   |||    | ||| |||  ||||||    |     | ||| |||| | |||| | | ||||||  | || |
   TTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAA
      630       640       650       660       670       680       690

         720       730       740       750       760       770       780
   ATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCG
     ||||||||||||||||||| |    |||  |||| |||||   ||||| ||| | |||       |   |
   TACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAG
    700       710       720       730       740       750       760

       790       800       810       820       830       840       850
   AACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTT
   |||   ||| |  |  | || || |    |      ||| | ||   |||||   || |
   AACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAAT---CCTGACTCGTTCCAAATACAACCAG
  770       780       790       800       810          820       830

     860       870       880       890       900       910             920
   ATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT------CAAGAAATAC
   |   |||   ||||| ||    ||     |||||||   |||   || ||||||||      |||     ||
   AACTCTAAATACATCAAC---TACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAAC
   840       850          860       870       880       890       900

         930       940       950       960       970       980       990
   GCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAA
    |       | ||| ||  | ||||| || ||  | ||     | ||| |  |  |  |      |||  |
   TCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAG
    910       920       930       940       950       960       970

      1000          1010      1020      1030      1040      1050      1060
   GAATACCGTCT----GGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCC
   ||||  ||| |      |||| | | ||||  ||   |  | ||||||| | ||    |||| |   ||| |
   GAATGGCGTGTATACACCTACAAGTACTTC-AAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCG---ATCTC
  980       990      1000       1010      1020      1030      1040

        1070      1080      1090      1100      1110         1120      1130
   GGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTA---TCACTAACAAATG
    ||    |   | || |   |     |    || |||    |  |||| |||   |    | ||  | |
   TGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCT
   1050      1060      1070      1080      1090      1100      1110

         1140      1150      1160      1170      1180      1190
   CAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAA------
        | ||     | ||  |   |  | |||| |||||| | |||||| ||||||  ||| || |
   GCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGG
 1120      1130      1140      1150      1160      1170      1180      1190

   1200                1210              1220            1230      1240
   TATCG----------CTAAACTGGTTGCT--------TCCAACTGGTAC------AATCGTCAGATCGAACG
   |||||           || |  |  | ||        ||||| ||||||       |   | |   | |||
TATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACC
      1200      1210      1220      1230      1240      1250      1260

  1250      1260      1270      1280      1290      1300      1310
TTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTA
 | |   |  |  |||||||||  |||| |||||||||||   || || ||||||   |||      |
GTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCT
    1270      1280      1290      1300      1310      1320      1330

1320  X
AGAATTC
||| |
AGAGTCGAGGCCTGCAG
  1340      1350
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-3-inv.res made by bobryen on Thu 7 Nov 102 14:40:46-PST.


Query sequence being compared:US-09-910-186A-3' (1-1323)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-3' (1-1323) with:
        File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                  *
N     -
C     -
E     -                                                              *
S     0--------------------------------------------------------------------
      |     ||      |      |      |      | |    | |    | |    |  |   |
SCORE 0     |6     12     18     24     31 |   37 |   43 |   49  |  55
STDEV      -6      -5     -4     -3       -2     -1      0       1


                           PARAMETERS

Similarity matrix       Unitary     K-tuple                 4
Mismatch penalty              1     Joining penalty        30
Gap penalty                5.00     Window size           500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                        SEARCH STATISTICS

Scores:                 Mean       Median     Standard Deviation
                          47         45             6.35

Times:                   CPU                  Total Elapsed
                     00:00:00.00               00:00:00.00

Number of residues:               4027
Number of sequences searched:        3
Number of scores above cutoff:       3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                      Init. Opt.
Sequence Name     Description                  Length Score Score  Sig. Frame
------------------------------------------------------------------------------
               ****  1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U  1351    55   429   1.26    0
               ****  0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U  1338    44   475  -0.47    0
  3. US-08-123-975A-1 Sequence 1, Application U  1338    44   475  -0.47    0


1. US-09-910-186A-3' (1-1323)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =     55  Optimized Score   =    429  Significance =  1.26
Residue Identity  =    40%  Matches           =    518  Mismatches   =   663
Gaps              =     89  Conservative Substitutions              =     0

   80        90       100       110       120       130       140       150
    CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAAACCGATG
                           | |   | |||  |   |  ||| ||  |  |     |        |
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X       10        20        30        40        50

          160       170       180       190       200       210       220
    AAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTCGTTCTTG
          | |  |  | || | |  ||   | |  |  ||  |    |     |||       | || | |||
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90       100       110       120

        230       240       250       260       270       280       290
    GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTTTTCTACA
     | |  ||  ||||  ||| |   || | |  |  | ||||  |  ||          ||||||  |  |||
    AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGTGTTAC-
       130       140        150       160       170                 180

      300       310       320       330       340       350       360
    CCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATACACGATCA
     |||  | |||| |||      | |  | |||||| | |         ||  |  || |   | |  ||||
    TCAGAATCAGAA-CATCATCTTCAACTCCGTATTCCTGG---------ACTTCTCTGTTTCCTTCTGGATCC
      190        200       210       220                230       240

    370       380       390         400       410       420       430
    TTGTTGCGAACGATATTGTCCTTGTTA-CCAGACGCGTATTTCTTGATGATGAATTTGGTACCACGGTACAG
     | |  ||||  | |    |   | || |||||     ||         ||  |       | || | |
    GTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGA
    250       260       270       280       290        300       310

    440       450           460        470       480       490      500
    GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCACGCGGACCTTTCAGGTACATGTAACCG
     ||| |  || |||    |||| |   |  |   |||| | | ||   ||||   || | |  || | | ||
    AGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGAC---TCTGATCGATATCAACG
   320       330       340       350       360       370          380

       510       520       530       540       550       560       570
    CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGTACGGTTTGTCG
       | ||| |   |||   | || |  ||     || |     |||   ||      ||   |  |   | |
    GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCGCTGG
   390       400       410        420       430          440       450

    580       590       600       610       620       630       640
    TACTGCAGGTAGTCACCCCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCTTTGATT
    | || |  ||   || | |  |   | |  |  || | | |||     |    ||  || |  | | ||
    TTCTTC--GTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATA
     460         470       480       490       500       510       520

  650       660             670        680         690       700       710
    TCTTTTTCGTTCAGTTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCGGTGAGTG
     |    ||    |  ||       || |||   |   ||||    | ||  | |  || |  |   |   |
    CCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATC
        530       540       550       560       570       580       590

          720       730       740       750       760             770
    TCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG------ATTGGAGATC
   ||      | ||  | |  || |       ||    | |   ||  |  | |||      || | ||| |
 GTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAAC
600       610       620       630       640       650       660       670

780       790       800          810        820       830       840
 GGTTTCTGGTCGATCAGACGGCCGTTGATGT---AGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTA
 |||    | || |        |||   |  |   ||| ||  | | || || |  |||        |    |
 GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGAT------GTACAACA
        680       690       700       710       720             730

 850       860       870       880       890       900       910
 ACGAAGATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTTTG
 | ||| |      | |  |||  |  |   |      | |  | | | |     || ||    || |   ||
 AAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTG
  740       750       760       770       780       790       800

920      930       940       950       960             970       980
 ATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCA------GAGATACTTTCCAACCAGAA
 |  |||||| |    | || |  | |   ||  ||    ||  |||      | ||    | |      |||
 AAATCCTGACT-CGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAA
810        820       830       840       850       860       870

   990             1000      1010      1020      1030      1040      1050
 TTGTTTTCCATGC-------AGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTATTTCGG
   |||   ||| |       |  | |   |       ||| || | | |  |   |    ||||  |
 AAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATC
880      890       900       910       920       930       940       950

            1060      1070      1080      1090      1100      1110
 GATACGGA-----TCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATACGATAGCATTCTTCAGG
  |   |||     || |   | |   |||   |  |   ||||   |   |||    | || |      ||
 TACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCA-AGAAAGAAGAAGA
       960       970       980       990      1000       1010      1020

1120      1130      1140      1150      1160      1170      1180
 ATAACTTCGATTTTGGAAGATTCCAGATTGAACAGCTGGATCTGATTCTTGTCGATCGGATCGAAGTTAAC-
 | | |||    |      |||  | ||||         || ||         |   | |||| |||   ||
 AAAGCTTTTCCTGGCTCCGATCTCTGATT----CCGACGAACTCTACAACACCATCCAGATCAAAGAATACG
     1030      1040      1050          1060      1070      1080      1090

1190        1200      1210      1220      1230      1240      1250
 -TTTAGAACCGA--TGTTGATTTTGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAG
     | | ||||  |  |  |    |  ||    | ||| || | ||  |    | ||      | |  | |
 ACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGAT-GAAGAATCTACTGACGAAATCGGTCTG
       1100      1110      1120      1130       1140      1150      1160

1260      1270      1280      1290      1300      1310      1320  X
 GTTCAGGATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGTAGACATCGTTTCGAATTC
  |           || |  | ||   |  |   ||||||   |||   | | |    |||    ||
 ATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAA
      1170      1180      1190      1200      1210      1220      1230

 TGGTACCTGAAGGA
    1240


2. US-09-910-186A-3' (1-1323)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     44  Optimized Score =     475  Significance = -0.47
Residue Identity  =    43%  Matches         =     583  Mismatches   =   677
Gaps              =     82  Conservative Substitutions          =     0

         10        20        30        40        50        60        70
 GAATTCTTACAGCGGACGTTCACCCCAACCGTCATCAACCGGGATGAACTCCCAAGAGCAACCCAGAGTGCG
                    ||   |||    || ||   | |  |    || |   |   | | |||
                   CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
                   X       10         20        30        40        50

       80        90        100       110       120       130       140
 AGAGGAACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
 |     || | |   ||||       ||| |    | | | ||| |     |||     ||    | |  |
 ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
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      60        70                80        90        100       110

    150       160       170       180       190       200       210
 ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
  |     ||| | | |||| | | |  |||  | |   ||| |  |   ||    | ||    |  ||| ||
 GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGAATCAGATCCA-GCTGTTC
  120       130       140       150         160       170        180

  220       230       240       250       260       270       280
 GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
   ||| | || |    | | | |  | |  |   | |  || |     |  | | |    |   | ||
 AATCTGGAATCTTCCAAAATCGAAGTTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAAC
   190       200       210            220        230       240       250

290       300       310       320       330       340       350       360
 TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
 |||| ||||  | |     | ||  ||| ||   ||  || |||       | ||     |   ||| ||||
 TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
    260          270       280          290       300       310       320

            370       380       390       400        410        420
 ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
 || |||||    ||    |||    ||| |  |||  |     | | | | | |      || |  | |
 ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
        330       340       350       360       370       380       390

 430       440       450       460         470       480       490
 CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
 |  | | |||   | ||  |||   ||    | ||| ||  |||     |        || | || |  |||
 CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
      400       410       420       430       440       450       460

  500       510       520       530       540         550       560
 ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
 ||  | |   ||||     | | |||  | ||| |     |  || ||     | || | ||  |||  |
 ATCAATCGCTGGAT-----CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACG
    470            480       490       500       510       520       530

  570        580       590          600       610       620       630
 ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
  | || || |||  | | |     || ||   |  |    | | || | | | |  |      || |
 GCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAAC
       540       550       560       570       580       590       600

    640       650       660       670       680       690       700
 TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
 |  | |  | |  |  |  |  |    |  |||   || || |  |  |  | || ||   |||  |    |
 TGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACG
     610       620       630       640       650       660       670

  710       720       730       740       750       760       770
 TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
   |  |  |  | |  | |  |     | ||      |  | | | | || | |    |  |   || ||
 AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
   680       690       700       710       720       730          740

780       790       800       810       820       830       840       850
 GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTAACG
    | | |  ||| || || |   |  |||  || | || |     || ||  |     | ||| |  |||
 ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
    750        760       770       780         790       800       810

             860       870       880       890       900       910
 AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
 | |     ||||   | |  |||||  |    | | |   | |      || | ||| ||| |    ||
 ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
     820       830         840       850       860        870        880

 920       930       940       950       960       970       980
 TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
 |||  || |   ||| | |  |   ||| ||   |   |   |  |  | |     |  |||  | |||
 TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
      890       900        910       920       930       940       950
 990      1000      1010      1020      1030      1040         1050
   TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
    |||    ||    ||||| |||||| |||   |     || |       ||| ||    || || |||
   GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
       960           970       980       990      1000      1010      1020

     1060      1070      1080      1090      1100         1110      1120
   GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
    | | |  | |  |||| ||||    || |   |    | | |  |   ||      |  || |  | |  |
   TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
         1030      1040      1050      1060      1070      1080      1090

      1130      1140      1150       1160      1170        1180      1190
   CGATTTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
    | | |    | || | |||  || || | |    || |    ||   |  | |||   | |  |||  | |
   AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
       1100      1110      1120      1130      1140      1150      1160

       1200        1210      1220      1230      1240      1250      1260
   AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGTTCAG
    | |||| | | |||  | |      | |    ||     |||     | ||| | | |    | ||| ||
   TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
     1170      1180      1190      1200      1210      1220      1230

       1270      1280      1290      1300          1310      1320  X
   GATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGT----AGACATCGTTTCGAATTC
    || |    || ||  | |||| |   | | || | |  | |     ||  || |  ||  |
   -ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTT
     1240        1250      1260      1270      1280      1290      1300

   GGGGTGAACGTC
     1310


3. US-09-910-186A-3' (1-1323)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =     44  Optimized Score =     475  Significance = -0.47
Residue Identity  =    43%  Matches         =     583  Mismatches   =   677
Gaps              =     82  Conservative Substitutions              =     0

           10        20        30        40        50        60        70
   GAATTCTTACAGCGGACGTTCACCCCAACCGTCATCAACCGGGATGAACTCCCAAGAGCAACCCAGAGTGCG
                      ||   |||    || ||   | |  |    || |   |   | | |||
                     CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
                     X       10         20        30        40        50

         80        90       100       110       120       130       140
   AGAGGAACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
   |     || | |   ||||       ||| |    | | | ||| |     |||     ||    | |  |
   ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
        60        70               80        90       100       110

      150       160       170       180       190       200       210
   ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
    |     ||| | | |||| | | |  |||  | |   ||| |  |   ||    | ||    |  ||| ||
   GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGAATCAGATCCA-GCTGTTC
    120       130       140       150         160       170        180

    220       230       240       250       260       270       280
   GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
     ||| | || |    | | | |  | |  |   | |  || |     |  | | |    |   | ||
   AATCTGGAATCTTCCAAAATCGAAGTTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAAC
     190       200       210          220       230       240       250

  290       300       310       320       330       340       350       360
   TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
   |||| ||||  | |     | ||  ||| ||   ||  || |||       | ||     |   ||| ||||
   TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
      260          270       280          290       300       310       320

              370       380       390       400        410       420
   ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
   || |||||    ||    |||    ||| |  |||  |     | | | | | |      || |  | |
   ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
          330       340       350       360       370       380       390

   430       440       450       460         470       480       490
   CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
   |  | | |||   | ||  |||   ||    | ||| ||  |||     |        || | || |  |||
   CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
        400       410       420       430       440       450       460

    500       510       520       530       540         550       560
   ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
   ||  | |   ||||     | | |||  | ||| |     |  || ||     | || | ||  |||  |
   ATCAATCGCTGGAT-----CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACG
      470            480       490       500       510       520       530

    570        580       590          600       610       620       630
   ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
    | || || |||  | | |     || ||   |  |    | | || | | | |  |      || |
   GCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAAC
         540       550       560       570       580       590       600

      640       650       660       670       680       690       700
   TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
   |  | |  | |  |  |  |  |    |  |||   || || |  |  |  | || ||   |||  |    |
   TGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACG
       610       620       630       640       650       660       670

    710       720       730       740       750       760       770
   TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
     |  |  |  | |  | |  |     | ||      |  | | | | || | |    |  |   || ||
   AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
     680       690       700       710       720       730          740

  780       790       800       810       820       830       840       850
   GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTAACG
      | | |  ||| || || |   |  |||  || | || |     || ||  |     | ||| |  |||
   ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
      750        760       770       780         790       800       810

               860       870       880       890       900       910
   AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
   | |     ||||   | |  |||||  |    | | |   | |      || | ||| ||| |    ||
   ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
       820       830         840       850       860        870       880

   920       930       940       950       960       970       980
   TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
   |||  || |   ||| | |  |   ||| ||   |   |   |  |  | |     |  |||  | |||
   TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
        890       900        910       920       930       940       950

 990      1000      1010      1020      1030      1040         1050
   TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGGATAC---
    |||    ||    ||||| |||||| |||   |     || |       ||| ||    || || |||
   GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
       960           970       980       990      1000      1010      1020

     1060      1070      1080      1090      1100         1110      1120
   GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
    | | |  | |  |||| ||||    || |   |    | | |  |   ||      |  || |  | |  |
   TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
         1030      1040      1050      1060      1070      1080      1090

      1130      1140      1150       1160      1170        1180      1190
   CGATTTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
    | | |    | || | |||  || || | |    || |    ||   |  | |||   | |  |||  | |
   AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
       1100      1110      1120      1130      1140      1150      1160

       1200        1210      1220      1230      1240      1250      1260
   AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGTTCAG
 | |||| | | |||  | |      | |    ||     |||     | ||| | | |    | ||| ||
TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
 1170      1180      1190      1200      1210      1220      1230

   1270      1280      1290      1300          1310      1320  X
GATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGT----AGACATCGTTTCGAATTC
 || |    || ||  | |||| |   | | || | |  | |     ||  || |  ||  |
-ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTT
 1240        1250      1260      1270      1280      1290      1300

GGGGTGAACGTC
 1310
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-4.res made by bobryen on Thu 7 Nov 102 14:32:06-PST.


Query sequence being compared:US-09-910-186A-4 (1-434)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

      Results of the initial comparison of US-09-910-186A-4 (1-434) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -                          * *                                 *
S    0---------------------------------------------------------------------
      |      |  |   |      |      |  |   |      |      | |    |      |
SCORE 0     46  |  92    139    185  | 231    277    324 | 370    416
STDEV          -1                    0                   1

                          PARAMETERS

Similarity matrix       PAM-150     K-tuple               1
Threshold level of sim.     16%
Mismatch penalty              1     Joining penalty      20
Gap penalty                5.00     Window size         434
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                       SEARCH STATISTICS

Scores:                 Mean       Median      Standard Deviation
                         263        181         132.66

Times:                  CPU                    Total Elapsed
                   00:00:00.00                 00:00:00.00

Number of residues:                   1704
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                            Init. Opt.
Sequence Name     Description                        Length Score Score  Sig. Frame
-----------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
  1. US-08-123-975A-3 Sequence 3, Application U    415   416   416   1.15   0
                    ****  0 standard deviation from mean ****
  2. US-08-123-975A-5 Sequence 5, Application U    439   193   273  -0.53   0
  3. US-08-123-975A-2 Sequence 2, Application U    850   180   275  -0.63   0


1. US-09-910-186A-4 (1-434)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =    416  Optimized Score  =    416  Significance =  1.15
Residue Identity =    100%  Matches          =    415  Mismatches   =     0
Gaps              =      0  Conservative Substitutions              =     0

          10        20        30        40        50        60        70
  MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||
                     RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
                     X       10        20        30        40        50

        80        90       100       110       120       130       140
  NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMIN
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMIN
       60        70        80        90       100       110       120

     150       160       170       180       190       200       210
  ISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  ISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKE
    130       140       150       160       170       180       190

   220       230       240       250       260       270       280
  LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYL
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  LNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYL
  200       210       220       230       240       250       260

 290       300       310       320       330       340       350       360
  NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
270       280       290       300       310       320       330       340

         370       380       390       400       410       420       430
  MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
  MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
        350       360       370       380       390       400       410

   X
  PL
  ||
  PL
   X


2. US-09-910-186A-4 (1-434)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =    193  Optimized Score  =    273  Significance = -0.53
Residue Identity =     38%  Matches          =    169  Mismatches   =   230
Gaps              =     17  Conservative Substitutions              =    26

     X    10        20        30        40        50        60        70
  MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY
     |  |   | |  ||||||  | ||||| |::|: :   |     ||||  |     ||| |     |::
     FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNIIF
     X       10        20        30        40          50        60
```

```
         80        90          100       110       120       130       140
   NSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
   || :  || ||||||||| |        ||||||||| ||||||:|     ||||| |       | | |
   NSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNI
    70        80        90       100       110       120       130

         150       160       170       180       190       200       210
   MINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLF
      ||:||||| ||||||| |||:||||||:|     |     : |   | |||||  |   :|| |||  |
   REDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIF
 140       150        160       170       180       190       200       210

       220       230       240       250       260       270       280
   DKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTN
     ||    | : |  || |  ||||||  | | | ||| |    | |:        |    :
   NTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYI
          220       230       240       250       260       270       280

     290       300       310       320       330       340       350
   IYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ
    |             |  :    | |||  | :|      | | |  |       |  |    | |
   NYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYN
        290       300       310       320       330       340       350

   360        370       380       390       400               410
   VVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA--------SNWYNRQIERS--SRTLGC
    :  |   :|            :    :|| || | |   :            | || : : |      |||
   TIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGC
      360       370       380       390       400       410       420

  420       430
   SWEFIPVDDGWGERPL
    | ||| |:|| |
   NWQFIPKDEGWTE
    430        X

3. US-09-910-186A-4 (1-434)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    180  Optimized Score =     275  Significance = -0.63
Residue Identity  =    37%  Matches         =     169  Mismatches   =   233
Gaps              =     17  Conservative Substitutions             =    26

                       X       10        20        30        40        50
                       MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQI
                          |  |   | |  ||||||  | ||||| |::|: :   |     ||||
   KYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQF
  390       400       410       420       430       440       450

         60        70        80        90          100       110       120
   QLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEI
    |     ||| |     |::|| :  || ||||||||| |        ||||||||| ||||||:|     |
   KLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRI
  460       470       480       490       500       510       520       530

         130       140       150       160       170       180       190
   IWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMF
   |||| |       | | |     ||:||||| ||||||| |||:||||||:|     |     : |   | |
   IWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIF
          540       550       560        570       580       590       600

       200       210       220       230       240       250       260
   KLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNN
   ||||  |   :|| |||  |  ||    | : |  || |  ||||||  | | | ||| |    | |:
   KLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKK
         610       620       630       640       650       660       670

     270       280       290       300       310       320       330
   VGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQ
       |    :           |             |  :    | |||  | :|      | | |  |
   DSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYF
```

```
       680       690       700       710       720       730       740

   340       350       360        370       380       390       400
   AGVEKILSALEIPDVGNLSQVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA-------
      |  |    | |       :  |   :|            :    :|| || | |   :
   KKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFC
     750       760       770       780       790       800       810

          410         420          X
   -SNWYNRQIERS--SRTLGCSWEFIPVDDGWGERPL
    | || : : |      ||| | ||| |:|| |
   ISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
   820       830       840       850
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5.res made by bobryen on Thu 7 Nov 102 14:41:38-PST.


Query sequence being compared:US-09-910-186A-5 (1-1326)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-5 (1-1326) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                          *
S    0----------------------------------------------------------------------
      |      |      |     | |      |      |     ||      |      |      |
SCORE 0    145    289    434    579    723    868   1013   1157   1302
STDEV                   -1                      0

                              PARAMETERS

Similarity matrix      Unitary     K-tuple                    4
Mismatch penalty             1     Joining penalty           30
Gap penalty               5.00     Window size              500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                   Mean       Median      Standard Deviation
                          1047        539         441.10

Times:                 CPU                       Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:                     4027
Number of sequences searched:              3
Number of scores above cutoff:             3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                                Init. Opt.
Sequence Name     Description                           Length Score Score   Sig. Frame
---------------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338  1302  1307   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U   1338  1302  1307   0.58    0
                  ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351   538   704  -1.15    0


1. US-09-910-186A-5 (1-1326)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =    1302  Optimized Score   =   1307  Significance =  0.58
Residue Identity =     98%  Matches           =   1311  Mismatches   =    15
Gaps             =       5  Conservative Substitutions                =     0

         X       10        20        30        40        50        60
         GAATTCGAAACGATGGCCTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
         |   | |      ||   |||||||||||||||||||||||||||||||||||||||||||||||||
    CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
         X  10        20        30        40        50        60        70

     70        80        90       100       110       120       130
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
          80        90       100       110       120       130       140

  140       150       160       170       180       190       200       210
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
       150       160       170       180       190       200       210

          220       230       240       250       260       270       280
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
     220       230       240       250       260       270       280

        290       300       310       320       330       340       350
    ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
   290       300       310       320       330       340       350       360

      360       370       380       390       400       410       420
    TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
           370       380       390       400       410       420       430

    430       440       450       460       470       480       490
    AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
         440       450       460       470       480       490       500

  500       510       520       530       540       550       560       570
    TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
       510       520       530       540       550       560       570

          580       590       600       610       620       630       640
    ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
     580       590       600       610       620       630       640

        650       660       670       680       690       700       710
    TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
   650       660       670       680       690       700       710       720

      720       730       740       750       760       770       780
    TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
            730       740       750       760       770       780       790

    790       800       810       820       830       840       850
    ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
         800       810       820       830       840       850       860

  860       870       880       890       900       910       920       930
    TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
       870       880       890       900       910       920       930

          940       950       960       970       980       990      1000
    GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
     940       950       960       970       980       990      1000

      1010      1020      1030      1040      1050      1060      1070
    GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
  1010      1020      1030      1040      1050      1060      1070      1080

     1080      1090      1100      1110      1120      1130      1140
    ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
            1090      1100      1110      1120      1130      1140      1150

   1150      1160      1170      1180      1190      1200      1210
    AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
        1160      1170      1180      1190      1200      1210      1220

  1220      1230      1240      1250      1260      1270      1280      1290
    CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
      1230      1240      1250      1260      1270      1280      1290

          1300      1310      1320          X
    ATGACGGTTGGGGTGAACGTCCGCTGTAA-----GAATTC
    |||||||||||||||||||||||||||||     |||  |
    ATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
    1300      1310      1320      1330      X


2. US-09-910-186A-5 (1-1326)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =   1302  Optimized Score  =   1307  Significance =  0.58
Residue Identity  =    98%  Matches          =   1311  Mismatches   =    15
Gaps              =      5  Conservative Substitutions              =     0

              X        10        20        30        40        50        60
              GAATTCGAAACGATGGCCTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
              |   | |      ||   |||||||||||||||||||||||||||||||||||||||||||||||||
         CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
              X  10        20        30        40        50        60        70

     70        80        90       100       110       120       130
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
          80        90       100       110       120       130       140

  140       150       160       170       180       190       200       210
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
       150       160       170       180       190       200       210

          220       230       240       250       260       270       280
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
     220       230       240       250       260       270       280

       290       300       310       320       330       340       350
    ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAG
  290       300       310       320       330       340       350       360

     360       370       380       390       400       410       420
    TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCA
            370       380       390       400       410       420       430

    430       440       450       460       470       480       490
    AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTC
         440       450       460       470       480       490       500

  500       510       520       530       540       550       560       570
    TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCC
       510       520       530       540       550       560       570

          580       590       600       610       620       630       640
    ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACT
     580       590       600       610       620       630       640

       650       660       670       680       690       700       710
    TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
  650       660       670       680       690       700       710       720

      720       730       740       750       760       770       780
    TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
            730       740       750       760       770       780       790

    790       800       810       820       830       840       850
    ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTA
         800       810       820       830       840       850       860

  860       870       880       890       900       910       920       930
    TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
       870       880       890       900       910       920       930

          940       950       960       970       980       990      1000
    GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
    940       950       960       970       980       990      1000

      1010      1020      1030      1040      1050      1060      1070
   GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
 1010      1020      1030      1040      1050      1060      1070      1080

     1080      1090      1100      1110      1120      1130      1140
   ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
          1090      1100      1110      1120      1130      1140      1150

  1150      1160      1170      1180      1190      1200      1210
   AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTT
        1160      1170      1180      1190      1200      1210      1220

 1220      1230      1240      1250      1260      1270      1280      1290
   CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTG
    1230      1240      1250      1260      1270      1280      1290

        1300      1310      1320          X
   ATGACGGTTGGGGTGAACGTCCGCTGTAA-----GAATTC
   |||||||||||||||||||||||||||||     |||  |
   ATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
   1300      1310      1320      1330     X

3. US-09-910-186A-5 (1-1326)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    538  Optimized Score =    704  Significance = -1.15
Residue Identity =    55%  Matches         =    759  Mismatches   =   530
Gaps             =     71  Conservative Substitutions          =     0

           10        20        30        40        50        60        70
   GAATTCGAAACGATGGCCTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTG
                         | ||||   ||||||      | ||| | || |    |||||||||||||
                     ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTG
                     X       10        20        30        40        50

          80        90       100       110       120       130       140
   CGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAAC
   || ||| ||  |||  | |||||||| |||||| | |||| | | ||| |  |  |   | | |  ||
   CGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT--ATACGACGGT----
        60        70        80        90       100       110       120

       150       160       170       180       190       200       210
   TTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAG
    | || | ||  |||||||| ||| || | |||  |  |   |     || || |||   ||||  | |||
   GTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAAT
           130       140       150       160       170       180       190

     220       230       240       250       260       270       280
   AATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTC
    |    ||| | | ||||||  | | |    |||||||    ||||||||||||||||||||||||||||
   CAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAG
         200       210       220       230       240       250       260

   290                300       310       320       330       340       350
   AACTCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGG
   |||  |         |  |   |  ||||||||||||||||||||||||||||| | || || |||||||||
   AACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGG
       270       280       290       300       310       320       330

         360       370       380       390       400       410       420
   AAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTA
   ||  | ||  |   |         |||||||||||||||   || |   | |  |  |   |   |||  |
   AAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTC
     340       350       360       370       380       390       400

        430       440       450       460       470       480       490
   TTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAAT
   ||| |||||             |||||||||| ||||||||||||||||| ||||||||||||||||||| ||
   TTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAA-
   410       420       430       440       450       460       470

      500       510       520       530       540       550       560
   CGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAAC
      ||||| ||  | ||||||||||||||||    |||       | |     |||    |  |  || |
   --CCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAA
    480       490       500       510       520       530       540

    570       580       590       600       610       620       630
   ATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAA
    |   ||||     | | ||||| |||||||||||||||      ||   |  ||  | |||||||||| |||
   GTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAA
  550       560       570       580       590       600       610       620

  640       650       660       670       680       690       700       710
   TACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCT
   ||||||    | ||| |||  ||||||    |     | ||||| |||| | |||| | | ||||||  | ||
   TACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCC
          630       640       650       660       670       680       690

          720       730       740       750       760       770       780
   GGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGAT
   |    ||||||||||||||||||| |    |||  ||||  |||||   ||||| ||| |  |||       |
   GAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAAC
        700       710       720       730       740       750       760

        790       800       810       820       830       840       850
   CCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCT
     ||||   ||| |  |  | || || |    |      ||| | ||   |||||   || |
   AAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAAT---CCTGACTCGTTCCAAATACAAC
      770       780       790       800       810         820       830

      860       870       880       890       900       910             920
   GTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT------CAAGAAA
      |   |||   ||||| ||    ||     |||||||   |||   || |||||||||      |||
   CAGAACTCTAAATACATCAAC---TACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCT
       840       850          860       870       880       890       900

          930       940       950       960       970       980       990
   TACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAAC
    || |       | ||| ||  | ||||| || ||  | ||     | ||| |  |  |   |      |||
   AACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAAT
        910       920       930       940       950       960       970

      1000          1010      1020      1030      1040      1050      1060
   AAAGAATACCGTCT----GGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAAT
    | ||||  ||| |      |||| | | ||||  ||   |  |||||| | ||    |||| |   ||
   CAGGAATGGCGTGTATACACCTACAAGTACTTC-AAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCG---AT
     980       990      1000       1010      1020      1030      1040

        1070      1080      1090      1100      1110      1120         1130
   CCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTA---TCACTAACAA
   | | ||    |   | || |   |     |    || |||    |  |||| |||   |    | ||  | |
   CTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCA
      1050      1060      1070      1080      1090      1100      1110

         1140      1150      1160      1170      1180      1190
   ATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAA---
           | ||     | ||  |   |  | |||| |||||| | |||||| |||||||  ||| || |
   GCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATC
    1120      1130      1140      1150      1160      1170      1180

   1200                1210              1220      1230            1240
   ---TATCG----------CTAAACTGGTTGCT--------TCCAACTGGTAC------AATCGTCAGATCGA
      |||||           || |  |  | ||        ||||| ||||||       |   | |   | |
    TGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAA
   1190      1200      1210      1220      1230      1240      1250

      1250      1260      1270      1280      1290      1300      1310
    ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCT
    ||  | |   |  |  |||||||||  |||| |||||||||||   || || ||||||   |||      |
    ACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACC
 1260      1270      1280      1290      1300      1310      1320      1330

    1320     X
    GTAAGAATTC
       ||| |
    TCTAGAGTCGAGGCCTGCAG
         1340      1350
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-5-inv.res made by bobryen on Thu 7 Nov 102 14:41:54-PST.


Query sequence being compared:US-09-910-186A-5' (1-1326)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-5' (1-1326) with:
        File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U  50-
M     -
B     -
E     -
R     -
      -
O     -
F  10-
      -
S     -
E   5-
Q     -
U     -
E     -                                   *
N     -
C     -
E     -                                          *
S    0-------------------------------------------------
       |  ||   |    |    |    | |  | |  | |  |  |  |
SCORE  0  |6   12   18   24   31 |  37 |  43 |  49 |  55
STDEV     -6   -5   -4   -3     -2    -1     0     1

                         PARAMETERS

Similarity matrix     Unitary    K-tuple                  4
Mismatch penalty            1    Joining penalty         30
Gap penalty              5.00    Window size            500
Gap size penalty         0.33
Cutoff score                1
Randomization group         0

                      SEARCH STATISTICS

Scores:               Mean      Median      Standard Deviation
                        47        45           6.35

Times:                 CPU                  Total Elapsed
                 00:00:00.00                00:00:00.00

Number of residues:                4027
Number of sequences searched:         3
Number of scores above cutoff:        3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                   ****  1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351    55   430   1.26   0
                   ****  0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338    44   478  -0.47   0
  3. US-08-123-975A-1 Sequence 1, Application U   1338    44   478  -0.47   0


1. US-09-910-186A-5' (1-1326)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    55  Optimized Score   =    430  Significance =  1.26
Residue Identity =    40%  Matches           =    519  Mismatches   =   665
Gaps              =    89  Conservative Substitutions                =     0

    80        90       100       110       120       130       140       150
     CGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAAACCGATG
                            | |   | |||  |   |  ||| ||  |  |     |        |
                         ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                         X        10        20        30        40        50

           160       170       180       190       200       210       220
     AAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTCGTTCTTG
           | |  |  | || | |  ||   | |  |  ||  |    |     |||       | || | |||
     TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
            60        70        80        90       100       110       120

         230       240       250       260       270       280       290
     GATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTTTTCTACA
      | |  || ||||  ||| |   || | |  |  | ||||  |  ||          ||||||  |  |||
     AACTGAATGACAAGAACCAG-TTCAAACTGACCTCTTCCGCTAACTC---------TAAGATCCGTGTTAC-
        130       140        150       160       170                180

       300       310       320       330       340       350       360
     CCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATACACGATCA
      |||  | |||| |||      | |  | |||||| | |         ||  |  || |   | |  ||||
     TCAGAATCAGAA-CATCATCTTCAACTCCGTATTCCTGG---------ACTTCTCTGTTTCCTTCTGGATCC
       190        200       210       220                 230       240

     370       380       390       400       410       420       430
     TTGTTGCGAACGATATTGTCCTTGTTA-CCAGACGCGTATTTCTTGATGATGAATTTGGTACCACGGTACAG
      | |  ||||  | |    |   | || |||||     ||         ||  |       | || | |
     GTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGA
     250       260       270       280       290       300       310

    440       450           460        470       480       490       500
     GGAAGAGTTCAGGT----AGATGTTGGT-AGTCATAACAGAACCACGCGGACCTTTCAGGTACATGTAACCG
      ||| |  || |||    |||| |   |  |   |||| | | ||   ||||   || | |  || | | ||
     AGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGAC---TCTGATCGATATCAACG
    320       330       340       350       360       370          380

       510       520       530       540       550       560       570
     CGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGATCGTACAGATTCAGCATGTAGTACGGTTTGTCG
        | ||| |   |||   | || |  ||     || |     |||   ||      ||   |  |   | |
     GTAAGACCAAATCTGTATTCTTCGA-ATACAACATCCGTGAAGACA---TCTCTGAATACATCAATCGCTGG
     390       400       410        420       430          440       450

     580       590       600       610       620       630       640
     TACTGCAGGTAGTCACCCCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCGTACAGGTCTTTGATT
     | || |  ||   || | |  |   | |  |  || | | |||     |    |    || ||  | | ||
     TTCTTC--GTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATA
      460         470       480       490       500       510       520

    650       660             670       680          690       700       710
     TCTTTTTCGTTCAGTTC------TTTGTCGAACAGATTGAA---GTATTTGATCCAGATGTAGCGGTGAGTG
      |    ||    |  ||       || |||   |   ||||    | ||  | |  || |  |   |   |
     CCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATC
      530       540       550       560       570       580       590

          720       730       740       750       760             770
     TCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAG------ATTGGAGATC
   ||      | ||  | |  || |       ||    | |   ||  |  | |||       || | ||| |
 GTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAAC
600       610       620       630       640       650       660       670

780       790       800          810       820       830       840
 GGTTTCTGGTCGATCAGACGGCCGTTGATGT---AGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTA
 |||    | || |        |||   |  |   ||| ||  | | || ||  |  |||        |    |
 GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGAT------GTACAACA
        680       690       700       710       720             730

 850       860       870       880       890       900       910
 ACGAAGATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTTTG
 | ||| |      | |  |||  |  |   |      | |  | | | |     || ||    || |   ||
 AAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTG
  740       750       760       770       780       790       800

920       930       940       950       960             970       980
 ATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCA------GAGATACTTTCCAACCAGAA
 |  |||||| |    | || |  | |   ||  ||    ||  |||       | ||    | |      |||
 AAATCCTGACT-CGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAA
810       820       830       840       850       860       870

  990                 1000      1010      1020      1030      1040      1050
 TTGTTTTCCATGC-------AGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTATTTCGG
   |||   ||| |       |  | |   |       ||| || | | | |  |   |    ||||  |
 AAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATC
880       890       900       910       920       930       940       950

              1060      1070      1080      1090      1100      1110
 GATACGGA-----TCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATACGATAGCATTCTTCAGG
  |   |||     || |   | |   |||   |  |   ||||   |   |||    | | |      ||
 TACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCA-AGAAAGAAGAAGA
      960       970       980       990      1000      1010      1020

1120      1130      1140      1150      1160      1170      1180
 ATAACTTCGATTTTGGAAGATTCCAGATTGAACAGCTGGATCTGATTCTTGTCGATCGGATCGAAGTTAAC-
 | | |||    |      |||  | ||||    |    || ||          |   | |||| |||   ||
 AAAGCTTTTCCTGGCTCCGATCTCTGATT----CCGACGAACTCTACAACACCATCCAGATCAAAGAATACG
    1030      1040      1050          1060      1070      1080      1090

1190      1200      1210      1220      1230      1240      1250
 -TTTAGAACCGA--TGTTGATTTTGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAG
     | | ||||  |  |  |    |  ||    | ||| || | ||  |    | ||       | |  | |
 ACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGAT-GAAGAATCTACTGACGAAATCGGTCTG
      1100      1110      1120      1130      1140      1150      1160

1260      1270      1280      1290      1300      1310      1320      X
 GTTCAGGATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGTAGAGGCCATCGTTTCGAATTC
  |           || |  | ||   |  |   ||||||   |||   | || | |    | |   | |
 ATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAA
     1170      1180      1190      1200      1210      1220      1230

 TGGTACCTGAAGGAAGT
    1240      1250
```

2. US-09-910-186A-5′ (1-1326)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score    =    44  Optimized Score   =    478  Significance = -0.47
Residue Identity =   43%  Matches           =    582  Mismatches   =   681
Gaps             =    78  Conservative Substitutions             =     0
```

```
          10        20        30        40        50        60        70
 GAATTCTTACAGCGGACGTTCACCCCAACCGTCATCAACCGGGATGAACTCCCAAGAGCAACCCAGAGTGCG
                    ||   |||    || ||   | |  |    || |   |   | | |||
                   CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
                   X        10        20        30        40        50

        80        90       100       110       120       130       140
 AGAGGAACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
 |     || | |   ||||        ||| |    | | | ||| |     |||     ||    | |  |
 ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
```

```
    60        70                80        90       100       110

  150       160       170       180       190       200       210
 ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
  |     ||| | | |||| | | |  |||  | |   ||| | |  |   ||    | ||    |  ||| ||
 GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGAATCAGATCCA-GCTGTTC
  120       130       140       150       160       170       180

  220       230       240       250       260       270       280
 GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
   ||| | || |    | | |  | |  |   | |  || |     |  | | |    |   | ||
 AATCTGGAATCTTCCAAAATCGAAGTTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAAC
  190       200       210          220       230       240       250

290       300       310       320       330       340       350       360
 TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
 |||| |||| | |     | ||  ||| ||   ||  || |||       | ||      |   ||| ||||
 TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
   260          270       280          290       300       310       320

             370       380       390       400        410       420
 ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
 || |||||    ||    ||    ||| |  |||  |     | | | | | |      || |  | |
 ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
         330       340       350       360       370       380       390

430       440       450       460       470       480       490
 CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
 |  | | |||   | ||  |||   ||     | ||| ||  |||     |        || | || |  |||
 CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
     400       410       420       430       440       450       460

 500       510       520       530       540           550       560
 ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
 ||  | |   ||||     | | |||  | ||| |     |  || ||     | || | ||  |||  |
 ATCAATCGCTGGAT-----CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACG
  470            480       490       500       510       520       530

 570       580       590          600       610       620       630
 ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
  | || || |||  | | |     || ||   |  |    | | || | | |  |      || |
 GCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAAC
      540       550       560       570       580       590       600

  640       650       660       670       680       690       700
 TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
 |  | |  | |  |  |  |  |    |  |||   || || | |  |  |  | || ||   |||  |    |
 TGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACG
   610       620       630       640       650       660       670

 710       720       730       740       750       760       770
 TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
   |  |  |  | |  | |  |     | ||      |  | | | | || | |    |  |   || ||
 AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
  680       690       700       710       720       730          740

780       790       800       810       820       830       840       850
 GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTAACG
    | | |  ||| || || |   |  |||  || | || |     || ||  |     |  ||| |  |||
 ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
   750       760       770       780         790       800       810

              860       870       880       890       900       910
 AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
 | |     ||||   | |  |||||  |    | | |   | |      || | ||| ||| |    ||
 ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
    820       830       840         850       860        870       880

 920       930       940       950       960       970       980
 TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
 |||  || |   ||| | |  |   ||| ||   |   |   |  |  | |     |  ||| | |||
 TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
      890       900        910       920       930       940       950
```

```
990      1000      1010      1020      1030      1040         1050
  TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGATAC---
   |||    ||    ||||| |||||| |||   |     || |       ||| ||    || || |||
  GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
      960           970       980       990      1000      1010      1020

   1060      1070      1080      1090      1100         1110      1120
  GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
   | | |  | |  |||| ||||    || |   |    | | |  |   ||      |  || |  | |  |
  TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
       1030      1040      1050      1060      1070      1080      1090

    1130      1140      1150       1160      1170        1180      1190
  CGATTTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
   | | |    | || | |||  || || | |    || |    ||   |  | |||   | |  |||  | |
  AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
     1100      1110      1120      1130      1140      1150      1160

     1200        1210      1220      1230      1240      1250      1260
  AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGTTCAG
   | |||| | | |||  | |      | |    ||     |||     | ||| | | |    | ||| ||
  TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
   1170      1180      1190      1200      1210      1220      1230

     1270      1280      1290      1300      1310      1320     X
  GATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGTAGAGGCCATCGTTTCGAATTC
   || |    || ||  | |||| |   | | || | |  | |   ||   |   | |   ||
  -ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTT
   1240        1250      1260      1270      1280      1290      1300

  GGGGTGAACGT
   1310


3. US-09-910-186A-5' (1-1326)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    44  Optimized Score =     478  Significance = -0.47
Residue Identity  =   43%  Matches         =     582  Mismatches   =   681
Gaps              =    78  Conservative Substitutions           =     0

          10        20        30        40        50        60        70
  GAATTCTTACAGCGGACGTTCACCCCAACCGTCATCAACCGGGATGAACTCCCAAGAGCAACCCAGAGTGCG
                     ||   |||    || ||   | |  |    || |   |   | | |||
                    CTCGAGCCATGGCTCGTC-TGCTGTCTACCTTCACTGAATACATCAAGAACATC
                    X       10         20        30        40        50

        80        90       100       110       120       130       140
  AGAGGAACGTTCGATCTGACGATTGTACCAGTTGGAAGCAACCAGTTTAGCGATATTGTTGAACTGGTGGAA
  |     || | |   ||||       ||| |    | | | ||| |     |||     ||    | |  |
  ATCAATACCTCCATCCTGA-------ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCT--AC
       60        70               80        90       100       110

     150       160       170       180       190       200       210
  ACCGATGAAACCGATATCGTTACCATTGTTGTCCTGCAGATTCATTTTGCATTTGTTAGTGATACCCTGGTC
   |     ||| | | |||| | | |  |||  | |   ||| |  |   ||    | ||    |  ||| ||
  GCTTCCAAAATCAACATCGGTTCTAAAGTTAACTT--CGATCCGATCGACAAGAATCAGATCCA-GCTGTTC
   120       130       140       150         160       170        180

   220       230       240       250       260       270       280
  GTTCTTGGATTTCATTACAACTACCTGAGACAGATTACCAACGTCCGGGATTTCCAGAGCAGACAAGATCTT
    ||| | || |    | | | |  | |  |   | |  || |     |  | | |    |   | ||
  AATCTGGAATCTTCCAAAATCGAAGTTATCC---TGAAGAATGCTATCGTATACAACTCTATGTACGAAAAC
    190       200       210          220       230       240       250

 290       300       310       320       330       340       350       360
  TTCTACACCAGCCTGAGAAGCATTGGTAGCCAGACGGTATTCTTTGTTCTTAACTACAACATTGATGTATAC
  |||| ||||  | |     | ||  ||| ||   ||  || |||       | ||     |   ||| ||||
  TTCTCCACCTCCTT---CTGGATCCGTATCC---CGAAATACTTCAACTCCATCTCTCTGAACAATGAATAC
     260          270       280          290       300       310       320

             370       380       390       400        410       420
  ACGATCAT----TGTTGCGAACGATATTGTCCTTGTTACCAGACGC-GTATTTCTTGATGATGAATTTGGTA
  || |||||    ||    |||    ||| |  |||  |     | | | | | |      || |  | |
  ACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACT
         330       340       350       360       370       380       390

  430       440       450       460         470       480       490
  CCACGGTACAGGGAAGAGTTCAGGTAGATGTTGGTAGTC--ATAACAGAACCACGCGGACCTTTCAG-GTAC
  |  | | |||   | ||  |||   ||    | ||| ||  |||     |        || | || |  |||
  CTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTAC
       400       410       420       430       440       450       460

   500       510       520       530       540         550       560
  ATGTAACCGCGGATACCTACATTGTTGACGTCAACGTATTTGTTCGGA--TCGTACAGATTCAGCATGTAGT
  ||  | |   ||||     | | |||  | ||| |     |  || ||     | || | ||  |||  |
  ATCAATCGCTGGAT-----CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACG
     470            480       490       500       510       520       530

   570        580       590          600       610       620       630
  ACGGTTTG-TCGTACTGCAGGTAGTCACC---CCAGAAGTCTTTCAGGATACCAGAATTGGACTGGTTGTCG
   | || || |||  | | |     || ||   |  |    | | || | | | |  |      || |
  GCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAAC
        540       550       560       570       580       590       600

     640       650       660       670       680       690       700
  TACAGGTCTTTGATTTCTTTTTCGTTCAGTTCTTTGTCGAACAGATTGAAGTATTTGATCCAGATGTAGCGG
  |  | |  | |  |  |  |  |    |  |||   || || |  |  |  | || ||   |||  |    |
  TGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACG
      610       620       630       640       650       660       670

   710       720       730       740       750       760       770
  TGAGTGTCACGACAACCGTCCAGTTTGAACATGATGTTATTAGAAGCGTGGATGTTACCCAGATTGGAGATC
    |  |  |  | |  | |  |     | ||      |  | | | | || | |    |  |   || ||
  AAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGG---GGTGACT
    680       690       700       710       720       730          740

 780       790       800       810       820       830       840       850
  GGTTTCTGGTCGATCAGACGGCCGTTGATGTAGATTTTGGAGTTATTCAGACGATTGTTGGTGATGGTAACG
     | | |  ||| || || |   |  |||  || | || |     || ||  |     | ||| |  |||
  ACCTGCAGTACGA-CAAACCGTACTACATGCTGAATCTGTA--CGATCCGAACAAATACGTTGACGTCAACA
     750        760       770       780         790       800       810

              860       870       880       890       900       910
  AAG-----ATCCAGCGATTGATGTAGTCAGAGATGTTGATCATCTGAGAGTATTTGAATACAACACGCTGTT
  | |     ||||   | |  |||||  |    | | |   | |      || | ||| ||| |    ||
  ATGTAGGTATCCGCGGTTACATGTA--CCTGAAAGGTCCGCGTGGTTCTGT-TATGACTACCAACATCTACC
      820       830         840       850       860        870       880

  920       930       940       950       960       970       980
  TGATTTCCTGAGTGTCCTGCAGAGTCCAGATGATTTCACCGTAGTTCAGAGATACTTTCCAACCAGAATTGT
  |||  || |   ||| | |  |   ||| ||   |   |   |  |  | |     |  |||  | |||
  TGAACTCTTCCCTGTACCG-TGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATC
       890       900        910       920       930       940       950

990      1000      1010      1020      1030      1040         1050
  TTTCCATGCAGTTGATGATGGTGTATTCATTGTTCAGAGAGATGGAGTTGAAGTAT---TTCGGATAC---
   |||    ||    ||||| |||||| |||   |     || |       ||| ||    || || |||
  GTTCGCAACA----ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAA
      960           970       980       990      1000      1010      1020

   1060      1070      1080      1090      1100         1110      1120
  GGATCCAGAAGGAGGTGGAGAAGTTTTCGTACATAGAGTTGTATAC---GATAGCATTCTTCAGGATAACTT
   | | |  | |  |||| ||||    || |   |    | | |  |   ||      |  || |  | |  |
  TGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGT
       1030      1040      1050      1060      1070      1080      1090

    1130      1140      1150       1160      1170        1180      1190
  CGATTTTGGAAGATTCCAGATTGAACA-GCTGGATCTGATTCTTGTCGATCGGATC--GAAGTTAACTTTAG
   | | |    | || | |||  || || | |    || |    ||   |  | |||   | |  |||  | |
  AGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
     1100      1110      1120      1130      1140      1150      1160

     1200        1210      1220      1230      1240      1250      1260
  AACCGATGTTGATTT--TGGAAGCGTAGCGAGACAGGTCGATCAGGTGATTGGATTCGTAGCGCAGGTTCAG
 | |||| | | |||  | |      | |    ||     |||     | ||| | | |    | ||| ||
TAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACA-
 1170      1180      1190      1200      1210      1220      1230

   1270      1280      1290      1300      1310      1320     X
GATGGAGGTATTGATGATGTTCTTGATGTATTCAGTGAAGGTAGAGGCCATCGTTTCGAATTC
 || |    || ||  | |||| |   | | || | |  | |   ||   |   | |   ||
-ATCGTCAGATCGA--ACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTT
 1240        1250      1260      1270      1280      1290      1300

GGGGTGAACGT
 1310
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-6.res made by bobryen on Thu 7 Nov 102 14:32:29-PST.


Query sequence being compared:US-09-910-186A-6 (1-435)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-6 (1-435) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -                        * *                              *
S    0---------------------------------------------------------------
      |     |  |   |     |     |  |   |     |      | |   |      |
SCORE 0    46  |  92   139   185  | 231   277    324 | 370    416
STDEV         -1                  0                  1


                           PARAMETERS

Similarity matrix       PAM-150    K-tuple                  1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty         20
Gap penalty               5.00     Window size            435
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                          SEARCH STATISTICS

Scores:                   Mean      Median      Standard Deviation
                           263        181        132.66

Times:                  CPU                     Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                     1704
Number of sequences searched:              3
Number of scores above cutoff:             3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                       Length Score Score  Sig. Frame
-----------------------------------------------------------------------------------
                      ****  1 standard deviation above mean ****
  1. US-08-123-975A-3 Sequence 3, Application U    415   416   416   1.15    0
                      ****  0 standard deviation from mean ****
  2. US-08-123-975A-5 Sequence 5, Application U    439   193   273  -0.53    0
  3. US-08-123-975A-2 Sequence 2, Application U    850   180   275  -0.63    0


1. US-09-910-186A-6 (1-435)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =    416  Optimized Score   =    416  Significance =  1.15
Residue Identity =    100%  Matches           =    415  Mismatches   =     0
Gaps              =      0  Conservative Substitutions               =     0

               10        20        30        40        50        60        70
       MASTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||
                           RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                           X       10        20        30        40        50

             80        90       100       110       120       130       140
       YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
             60        70        80        90       100       110       120

          150       160       170       180       190       200       210
       NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
          130       140       150       160       170       180       190

        220       230       240       250       260       270       280
       ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
        200       210       220       230       240       250       260

      290       300       310       320       330       340       350       360
       LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
      270       280       290       300       310       320       330       340

              370       380       390       400       410       420       430
       VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
              350       360       370       380       390       400       410

         X
       RPL
       |||
       RPL
         X


2. US-09-910-186A-6 (1-435)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =    193  Optimized Score   =    273  Significance = -0.53
Residue Identity =     38%  Matches           =    169  Mismatches   =   230
Gaps              =     17  Conservative Substitutions               =    26

           X   10        20        30        40        50        60        70
       MASTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
           |  |   | |  ||||||  | ||||| |::|: :   |     ||||  |     ||| |     |:
           FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNII
           X        10        20        30        40          50        60
          80        90          100       110       120       130       140
    YNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYS
    :|| :  || ||||||||| |        ||||||||| ||||||:|     ||||| |       | | |
    FNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYN
      70        80        90        100       110       120       130

          150       160       170       180       190       200       210
    QMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNL
        ||:||||| ||||||| |||:||||||:|     |     : |   | |||||  |   :|| |||
    IREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSI
   140       150        160       170       180       190       200

        220       230       240       250       260       270       280
    FDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTT
    |  ||    | : |  || |  ||||||  | | | ||| |    | |:        |    :
    FNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKY
  210       220       230       240       250       260       270       280

      290       300       310       320       330       340       350
    NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLS
      |             |  :    | |||  | :|      | | |  |       |  |    | |
    INYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFY
          290       300       310       320       330       340       350

    360       370        380       390       400             410
    QVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA--------SNWYNRQIERS--SRTLG
      :  |   :|            :    :|| || | |   :            | || : : |      ||
    NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLG
        360       370       380       390       400       410       420

   420       430 X
    CSWEFIPVDDGWGERPL
    | | ||| |:|| |
    CNWQFIPKDEGWTE
      430        X


3. US-09-910-186A-6 (1-435)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    180  Optimized Score  =     275  Significance = -0.63
Residue Identity =    37%  Matches          =     169  Mismatches   =   233
Gaps             =     17  Conservative Substitutions             =    27

                        X        10        20        30        40        50
                        MASTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQ
                        :   |  |   | |  ||||||  | ||||| |::|: :   |     ||||
    NKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQ
    390       400       410       420       430       440       450

          60        70        80        90          100       110       120
    IQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGE
      |     ||| |     |::|| :  || ||||||||| |        ||||||||| ||||||:|
    FKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNR
    460       470       480       490       500       510       520

          130       140       150       160       170       180       190
    IIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIM
    ||||| |       | | |     ||:||||| ||||||| |||:||||||:|     |     : |   |
    IIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEII
  530       540       550       560        570       580       590       600

        200       210       220       230       240       250       260
    FKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVN
    |||||  |   :|| |||  |  ||    | : |  || |  ||||||  | | | ||| |    | |:
    FKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLK
           610       620       630       640       650       660       670

      270       280       290       300       310       320       330
    NVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNAS
         |    :           |             |  :    | |||  | :|      | | |  |
    KDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKY
```

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     680       690       700       710       720       730       740

340       350       360       370        380       390       400
QAGVEKILSALEIPDVGNLSQVVVMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA------
    |  |    | |       :  |   :|            :    :|| || | |   :
FKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYF
   750       760       770       780       790       800       810

       410         420       430 X
--SNWYNRQIERS--SRTLGCSWEFIPVDDGWGERPL
  | || : : |      ||| | ||| |:|| |
CISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
 820       830       840       850
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-7.res made by bobryen on Thu 7 Nov 102 14:42:16-PST.


Query sequence being compared:US-09-910-186A-7 (1-1341)
Number of sequences searched:                         3
Number of scores above cutoff:                        3

      Results of the initial comparison of US-09-910-186A-7 (1-1341) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                         *
N     -
C     -
E     -                                                                *
S    0----------------------------------------------------------------------
      |    ||      |      |      |      |      |     ||      |      |
SCORE 0   147     293    440    587    733    880  1027|   1173   1320
STDEV      -1                     0                     1

                              PARAMETERS

Similarity matrix       Unitary     K-tuple                   4
Mismatch penalty              1     Joining penalty          30
Gap penalty                5.00     Window size             500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                              SEARCH STATISTICS

Scores:                   Mean        Median      Standard Deviation
                          795         534          454.37

Times:                  CPU                       Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                              Init. Opt.
Sequence Name     Description                          Length Score Score  Sig. Frame
--------------------------------------------------------------------------------------
                         ****  1 standard deviation above mean ****
   1. US-08-123-975A-6 Sequence 6, Application U   1351  1320  1323   1.16   0
                         ****  0 standard deviation from mean ****
   2. US-08-123-975A-4 Sequence 4, Application U   1338   533   699  -0.58   0
   3. US-08-123-975A-1 Sequence 1, Application U   1338   533   699  -0.58   0


1. US-09-910-186A-7 (1-1341)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =   1320  Optimized Score  =    1323  Significance =  1.16
Residue Identity  =    99%  Matches          =    1323  Mismatches   =    12
Gaps              =      0  Conservative Substitutions              =     0

          X 10        20        30        40        50        60        70
    GAATTCACGATGGCCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGAC
          | |     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGAC
          X       10        20        30        40        50        60

          80        90       100       110       120       130       140
    AACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAG
      70        80        90       100       110       120       130

       150       160       170       180       190       200       210
    AACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAAC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAAC
   140       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATTCGTATCCCGAAATACAAGAACGACGGTATCCAGAAT
    ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
    TCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAAT
           220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    TACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGT
         290       300       310       320       330       340       350

           370       380       390       400       410       420       430
    AACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    AACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGT
       360       370       380       390       400       410       420

         440       450       460       470       480       490       500
    GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
     430       440       450       460       470       480       490

       510       520       530       540       550       560       570
    TACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATC
   500       510       520       530       540       550       560       570

     580       590       600       610       620       630       640
    ATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACC
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACC
           580       590       600       610       620       630       640

   650       660       670       680       690       700       710       720
    GAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGG
        650       660       670       680       690       700       710

          730       740       750       760       770       780       790
   GGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTG
      720       730       740       750       760       770       780

        800       810       820       830       840       850       860
   AAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   AAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTAC
    790       800       810       820       830       840       850

      870       880       890       900       910       920       930
   CGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATC
  860       870       880       890       900       910       920       930

    940       950       960       970       980       990      1000
   GTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAG
          940       950       960       970       980       990      1000

 1010      1020      1030      1040      1050      1060      1070      1080
   TACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATC
       1010      1020      1030      1040      1050      1060      1070

         1090      1100      1110      1120      1130      1140      1150
   CAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACT
     1080      1090      1100      1110      1120      1130      1140

       1160      1170      1180      1190      1200      1210      1220
   GACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTAC
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTAC
   1150      1160      1170      1180      1190      1200      1210

     1230      1240      1250      1260      1270      1280      1290
   TTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTGCAATTGG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTGCAATTGG
 1220      1230      1240      1250      1260      1270      1280      1290

   1300      1310      1320      1330      1340
   CAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAAGAATTC
   |||||||||||||||||||||||||||||||||||||||    |
   CAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCCTGCAG
         1300      1310      1320      1330    X 1340      1350


2. US-09-910-186A-7 (1-1341)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    533  Optimized Score   =    699  Significance = -0.58
Residue Identity  =    55%  Matches           =    754  Mismatches   =   535
Gaps              =     71  Conservative Substitutions      =      0

                    X       10        20        30        40        50
                    GAATTCACGATGGCCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGA
                        |  | |    ||   ||||||      | ||| | || |    ||||||||
   CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
           10        20        30        40        50        60        70

      60        70        80        90       100       110         120
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   ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT--ATACGACGG
   ||||||| ||| ||  |||  | |||||||| |||||| | |||| | | ||| |  |  |   | | |  |
   ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
         80        90       100       110       120       130       140

         130       140       150       160       170       180       190
   T----GTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTC
   |     | || | ||  |||||||| ||| || | |||  |  |   |     || || |||   ||||  |
   TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
      150       160       170       180       190       200       210

       200       210       220       230       240       250       260
   AGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATTCGTATCCCGAAAT
    |||  |    ||| | | ||||||  | | |    |||||||    ||||||||||| |||||||||||||
   TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
    220       230       240       250       260       270       280

     270       280       290       300       310       320       330
   ACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTG
   ||   |||  |         |  |   |  ||||||||||||||||||||||||||||| | || || ||||
   ACTTCAACTCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTG
  290                300       310       320       330       340       350

   340       350       360       370       380       390       400
   GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTG
   |||||||  | ||  |   |         |||||||||||||||   || |   | |  |  |   |   ||
   GTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
         360       370       380       390       400       410       420

 410       420       430       440       450       460       470       480
   TATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCA
   |  | ||| |||||             |||||||||| ||||||||||||||| ||||||||||||||||||
   TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCA
       430       440       450       460       470       480       490

            490       500       510       520       530       540       550
   ATAA---CCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCC
   | ||    ||||| ||  | |||||||||||||||||    |||       | |     |||    |  |
   ACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGG
     500       510       520       530       540       550       560

          560       570       580       590       600       610       620
   GTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
   || |  |   ||||     | | ||||| |||||||||||||||      ||   |  ||  | ||||||||
   GTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGA
   570       580       590       600       610       620       630

        630       640       650       660       670       680       690
   TGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTT
   | |||||||||    | ||| |||  ||||||    |     | ||| |||| | |||| | | ||||||
   TCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCA
 640       650       660       670       680       690       700       710

      700       710       720       730       740       750       760
   ACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTG
   | || |    ||||||||||||||||||| |    |||  |||| |||||   ||||| ||| | |||
   ATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGT
         720       730       740       750       760       770       780

    770       780       790       800       810          820       830
   GTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAAT---CCTGACTCGTTCCAAAT
      |   ||||   ||| |  |  | || || |    |      ||| | ||   |||||   || |
   ACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTG
       790       800       810       820       830       840       850

     840       850       860          870       880       890       900
   ACAACCAGAACTCTAAATACATCAAC---TACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCA
           |   |||   ||||| ||    ||     |||||||   |||   || ||||||||      ||
   GTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT------CA
     860       870       880       890       900       910             920

      910       920       930       940       950       960       970
   AATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACC
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    |     || |       | ||| ||  | ||||| || ||  | ||     | ||| |  |  |  |
    AGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTA
          930       940       950       960       970       980       990

     980       990      1000      1010       1020      1030      1040
    TGAATCAGGAATGGCGTGTATACACCTACAAGTACTTC-AAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCG
     |||  | ||||  ||| |      |||| | | ||||  ||   |  | ||||||| | ||    |||| |
    AGAACAAAGAATACCGTCT----GGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTG
       1000      1010          1020      1030      1040      1050      1060

      1050      1060      1070      1080      1090      1100      1110
    ---ATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCT
       ||| | ||    |   | || |   |     |    || |||    |  |||| |||   |    | ||
    GAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTA---TCACT
         1070      1080      1090      1100      1110      1120         1130

    1120      1130      1140      1150      1160      1170      1180
    TGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTAC
      | |        | ||     | ||  |   |  | |||| |||||| | |||||| ||||||  ||| ||
    AACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAAC
          1140      1150      1160      1170      1180      1190      1200

  1190      1200      1210      1220      1230      1240      1250      1260
    GAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAA
     |      |||||           || |  |  | ||        ||||| ||||||       |   | |
    AA------TATCG----------CTAAACTGGTTGCT--------TCCAACTGGTAC------AATCGTCAG
                        1210      1220              1230            1240

          1270      1280      1290      1300      1310      1320      1330
    CGCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAG
      | |||  | |   |  |  |||||||||  |||| |||||||||||   || || ||||||   |||
    ATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGT
      1250      1260      1270      1280      1290      1300      1310

        1340
    TAAGAATTC
          |
    CCGCTGTAACCCGGGAAAGCTT
    1320    X 1330


3. US-09-910-186A-7 (1-1341)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    533  Optimized Score    =    699  Significance = -0.58
Residue Identity  =    55%  Matches            =    754  Mismatches   =   535
Gaps              =     71  Conservative Substitutions          =     0

                     X       10        20        30        40        50
                     GAATTCACGATGGCCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGA
                         |  | |    ||   ||||||      | ||| | || |    ||||||||
    CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
            10        20        30        40        50        60        70

       60        70        80        90       100       110         120
    ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT--ATACGACGG
    ||||||| ||| ||  |||  | |||||||| |||||| | |||| | | ||| |  |  |   | | |  |
    ACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAG
          80        90       100       110       120       130       140

          130       140       150       160       170       180       190
    T----GTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTC
    |     | || | ||  |||||||| ||| || | |||  |  |   |     || || |||   ||||  |
    TTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCC
       150       160       170       180       190       200       210

        200       210       220       230       240       250       260
    AGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATTCGTATCCCGAAAT
     |||  |    ||| | | ||||||  | | |    |||||||    ||||||||||| |||||||||||||
    TGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAAT
     220       230       240       250       260       270       280

      270       280       290       300       310       320       330

  ACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTG
  ||   |||  |         |  |   |  ||||||||||||||||||||||||||||| | || || ||||
  ACTTCAACTCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTG
 290                300       310       320       330       340       350

  340       350       360       370       380       390       400
  GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTG
  |||||||  | ||  |   |         |||||||||||||||   || |   | |  |  |   |   ||
  GTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
        360       370       380       390       400       410       420

410       420       430       440       450       460       470       480
  TATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCA
  |  | ||| |||||             |||||||||| ||||||||||||||| ||||||||||||||||||
  TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCA
      430       440       450       460       470       480       490

           490       500       510       520       530       540       550
  ATAA---CCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCC
  | ||    ||||| ||  | |||||||||||||||||    |||       | |     |||    |  |
  ACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGG
    500       510       520       530       540       550       560

         560       570       580       590       600       610       620
  GTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
  || |  |   ||||     | | ||||| |||||||||||||||      ||   |  ||  | ||||||||
  GTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGA
  570       580       590       600       610       620       630

       630       640       650       660       670       680       690
  TGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTT
  | |||||||||    | ||| |||  ||||||    |     | ||| |||| | |||| | | ||||||
  TCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCA
640       650       660       670       680       690       700       710

     700       710       720       730       740       750       760
  ACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTG
  | || |    ||||||||||||||||||| |    |||  |||| |||||   ||||| ||| | |||
  ATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGT
        720       730       740       750       760       770       780

   770       780       790       800       810          820       830
  GTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAAT---CCTGACTCGTTCCAAAT
     |   ||||   ||| |  |  | || || |    |      ||| | ||   |||||   || |
  ACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTG
      790       800       810       820       830       840       850

    840       850       860          870       880       890       900
  ACAACCAGAACTCTAAATACATCAAC---TACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCA
          |   |||   ||||| ||    ||     |||||||   |||   || ||||||||      ||
  GTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT------CA
    860       870       880       890       900       910             920

     910       920       930       940       950       960       970
  AATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACC
  |     || |       | ||| ||  | ||||| || ||  | ||     | ||| |  |  |  |
  AGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTA
        930       940       950       960       970       980       990

   980       990      1000      1010       1020      1030      1040
  TGAATCAGGAATGGCGTGTATACACCTACAAGTACTTC-AAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCG
   |||  | ||||  ||| |      |||| | | ||||  ||   |  | ||||||| | ||    |||| |
  AGAACAAAGAATACCGTCT----GGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTG
     1000      1010          1020      1030      1040      1050      1060

    1050      1060      1070      1080      1090      1100      1110
  ---ATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCT
     ||| | ||    |   | || |   |     |    || |||    |  |||| |||   |    | ||
  GAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTA---TCACT
       1070      1080      1090      1100      1110      1120         1130

  1120      1130      1140      1150      1160      1170      1180
  TGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTAC
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    | |     ||   ||   | ||  |   |  | |||| |||||| | |||||| ||||  ||| ||
  AACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAAC
        1140      1150      1160      1170      1180      1190      1200

1190      1200      1210      1220      1230      1240      1250      1260
  GAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAA
   |      ||||||           || |  |  | ||        ||||| ||||||       |   | |
  AA------TATCG----------CTAAACTGGTTGCT--------TCCAACTGGTAC------AATCGTCAG
                      1210      1220              1230            1240

        1270      1280      1290      1300      1310      1320      1330
  CGCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAG
    | |||  | |   |  |  |||||||||  |||| |||||||||||   || || ||||||   |||
  ATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGT
    1250      1260      1270      1280      1290      1300      1310

      1340
  TAAGAATTC
        |
  CCGCTGTAACCCGGGAAAGCTT
  1320    X 1330
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-7-inv.res made by bobryen on Thu 7 Nov 102 14:42:32-PST.

Query sequence being compared:US-09-910-186A-7' (1-1341)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-7' (1-1341) with:
        File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                  *
N     -
C     -
E     -                                                               *
S    0----------------------------------------------------------------------
      |     | |      |      |      |      ||     ||     ||     |  |   |
SCORE 0     | 6     12     18     24     30|    36|    42|    48  |  54
STDEV      -6       -5     -4     -3     -2     -1       0        1

                              PARAMETERS

Similarity matrix        Unitary        K-tuple                  4
Mismatch penalty               1        Joining penalty         30
Gap penalty                 5.00        Window size            500
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                           SEARCH STATISTICS

Scores:                   Mean        Median      Standard Deviation
                            46            44            6.35

Times:                     CPU                    Total Elapsed
                      00:00:00.00                 00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                        Init.  Opt.
Sequence Name     Description                    Length Score Score   Sig. Frame
--------------------------------------------------------------------------------
                  **** 1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351    54   488    1.26    0
                  **** 0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338    43   481   -0.47    0
  3. US-08-123-975A-1 Sequence 1, Application U   1338    43   481   -0.47    0


1. US-09-910-186A-7' (1-1341)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =     54  Optimized Score  =     488  Significance =  1.26
Residue Identity  =    41%  Matches          =     563  Mismatches   =   716
Gaps              =     90  Conservative Substitutions              =     0

                       X         10        20        30          40
                       GAATTCTT--ACTATTCGGTCC--AACCTTCGTCTTTCGGGATGAACTGCCA
                       ||| || |  || ||    |||  ||||| |||      |     | |   |
   CTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAATCTGA
       10        20    X   30        40        50        60        70

   50        60        70        80        90           100       110
   ATTGCAACCCAGTTTCAGGTTGTACGGTTTGCGTTTA--ACTTCCTTCA--GGTACCATTTGGAGATGCAGA
            | | ||  |||  ||  |||   || ||  ||    || |   | |  |   | |   |   |
   TCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAGTTCA
     80        90       100       110      120       130       140

    120       130       140       150       160       170       180
   AGTAGTCTTTGTATTCTTCGAATACGATACCAGATTCGTAGAAACGGTGGATACCGATCAGACCGATTTCGT
   |   | | |  |   ||     || ||| |  | | |  |||| | |   ||     |||   |  | |
   AACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCC
  150       160       170       180       190       200       210       220

  190       200       210       220       230       240       250
   CAGTAGATTCTTCATCTTTCTTGAACAGCAGCTGGCAAGAGTAGGTCGGCTGTTCGTCGTATTCTTT-----
     |     |||   || |||| || | | | |  | || |  ||  || | ||     | |||   |
   TGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACA
          230       240       250       260       270       280       290

               260       270       280       290        300       310
   ----------GATCTGGATGGTGTTGTAGAGTTCGTCGGAATCAGAGATC-GGAGCCAGGAAAAGCTTTTCT
              |||   |      || ||| |   || |  |   |||||   | ||  |  || | | ||
   ATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCA
        300       310       320       330       340       350       360

    320       330       340       350       360                370
   TCTTCTTTCTTGAAGTACTTGTAGGTGTATACACGCCATTCCTGATTCA---------GGTTGAAGAAGTCC
   |||    |||    |   |    |||     ||   |  |  |  |  |            ||||||  ||
   TCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGTGAAGACATCT
    370       380       390       400       410       420       430

  380       390       400       410       420        430       440
   AGGTAGATGTAGTCTTCTTTACGTACGATGTCATCATTGATGGACTG---AGAGTTAGATTTGCGACGGATG
     | | |  |      ||     | || |  |||||   ||   |||   |  | || | |    |   | |
   CTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACG
    440       450       460       470       480       490       500

  450       460       470       480       490       500       510       520
   ATGAACTTTTCACCGATGTACAGGTCGCGGTAGTTGATGTATTTAGAGTTCTGGTTGTATTTGGAACGAGTC
    | ||||     |  ||    |  ||   |   |   || | |||  | |   | || | |       |  |
   GTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAAC
  510       520       530       540       550       560       570       580

           530       540       550       560       570       580       590
   AGGATTTCACCAACCGGAGAGTCTTTCTTCAGTTTGATGTAAGAGTTCTTGTTACCAGCATTGAACATATAG
    |||      | | ||      |    ||||  | |||| || | ||||      |    || ||||   |
   TGGACGGTGAC-ATCGATCGTACCCAGTTCATCTGGATGAAATACTTCT------CCATCTTCAACACCGAA
           590       600       610       620            630       640

        600       610       620          630       640       650       660
   TATTCTTTGTTGTACATCAGCGGATTACCCCAGA---AGTCTTTCAGGTATTCGGAGTAAGACTGGATCTTG
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       |||  ||   | |||   | |     | |||   |||||| |    | |    | ||||||   ||| |
    CTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACT---TCTGG
      650       660       670       680       690       700          710

          670       680       690       700             710       720
    TACCGTTCTTCGATATTGGACTGAGACAGTTCGGTGTTGAA------GATGGAGAAGTATTTCATCCAGATG
         | |   ||| |   ||  |||    |   |||| ||       |   |||| | || |||| |  ||
    GGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTG
       720       730       740       750       760       770       780

     730       740       750       760       770       780       790
    AA-CTGGGTACGATCGATGTCACCGTCCAGTTTGAAGATGATTTCACCGTTAGCGATAACTTCACGGATGTC
    ||    |   |    | ||      ||| |  |       | | || |   | |  ||| | ||   |   |
    AAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTAC
     790       800       810       820       830       840       850

   800       810       820       830       840       850       860       870
    TTTGATGTCGGTATTAGATTCCAGTTTACCGTTGATGTAGATTTTAGCATTGTTCAGGTTATTGGTGATGGT
       ||  |    ||  |     |||| | | |   |    | | || |     ||||   ||   |||||
    CGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAAC---TCTCAGTCCATCAATGATGAC
   860       870       880       890       900          910       920

           880       890       900       910       920       930       940
    AACGAAGAACCAGCGATTGATGTATTCAGAGATGTCTTCACGGATGTTGTATTCGAAGAATACAGATTTGGT
    | || |     ||      |  | | |   ||  ||||||            |  |  |  |  |   ||
    ATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCA---------ACCTGAATCAGGAATGGCGTGTA
    930       940       950       960                970       980       990

         950       960       970       980       990      1000      1010
    CTTACCGTTGATATCGATCAGAGTCCAGATGATACGGTTACCGCGGATGGAGATCTTCCAACCAGAGTTATT
       |||    |   |    |||    ||| || | | ||  |  || |   |||||   |  | ||   | |
    TACACCTACAAGTACTTCAAGAAAGAAGAAAAGCTTTTCCTGGCT-CCGATCTCTGATTCCGACGAACT
          1000      1010      1020      1030       1040      1050      1060

      1020      1030      1040      1050      1060      1070      1080
    CTTCATGCAGTTGATGATGGTGTATTCATTGTGGATGTAATTCTGGATACCGTCGTTCTTGTATTTCGGGAT
    || ||      |   |||                |   ||| |     || | ||  ||  | || |  | |
    CTACAACACCATCCAGAT----------------CAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCT
         1070                     1080      1090      1100      1110

    1090      1100      1110      1120      1130      1140      1150
    ACGAATCCAGAAGGAAACAGAGAAGTCCAGGAATACGGAGTTGAAGATGATGTTCTGATTCTGAGTAACACG
     |   || |||| ||   |||     |     | |  |   |||     ||   | | ||||  | | |  |
    GCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGG
  1120      1130      1140      1150      1160      1170      1180      1190

  1160      1170      1180      1190      1200      1210      1220      1230
    GATCTTAGAGTTAGCGGAAGAGGTCAGTTTGAACTGGTTCTTGTCATTCAGTTCAACACCGTCGTATACTTC
     ||| ||     ||   |  | | |   ||   |   | |   |  |  |  | ||    ||  || ||
    TATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGT--ACCTGAAGGAAGT--TAAACGCA
          1200      1210      1220      1230        1240      1250

          1240      1250      1260      1270      1280      1290        1300
    AACTTTAGCACCGTAACCAGACAGATCGATCAGATTGTTGTCTTTGTAACGCAGGTTCAGGATGATATT--G
    |||  ||  |||  || | |         |   | |     |      ||| |||||       ||| |
    AACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAAC
  1260      1270      1280      1290      1300      1310      1320      1330

          1310         X      1330      1340
    TTCAGGATTTCGGAATTGTATTTGTTGGCCATCGTGAATTC
     ||  || |   |   || |
    CTCTAGAGTCGAGGCCTGCAG
          1340      1350


2. US-09-910-186A-7' (1-1341)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     43  Optimized Score =    481  Significance = -0.47
Residue Identity =     42%  Matches         =    577  Mismatches   =   716
Gaps             =     79  Conservative Substitutions           =     0

             10 X      20        30        40        50        60        70
    GAATTCTTACTATTCGGTCCAACCTTCGTCTTTCGGGATGAACTGCCAATTGCAACCCAGTTTCAGGTTGTA
                 |||  |||    ||||||   |          |  | | || |              ||
                CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATA
                X       10        20        30        40        50        60

          80        90       100       110       120       130       140
    CGGTTTGCGTTTAACTTCCTTCAGGTACCATTTGGAGATGCAGAAGTAGTCTTTGTATTCTTCGAATA-CGA
    |      | |  | || |  |  |   ||| |   |  ||    |   ||||   ||  |||| || | | |
    CCTCCATCCTGAACCTGCGCTACGAATCCAAT--CACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAA
            70        80        90         100       110       120       130

        150       160          170        180       190       200       210
    TACCAGATTCGTAGAAACGGTGGAT---ACCGATCAG-ACCGATTTCGTCAGTAGATTCTTCATCTTTCTTG
     | | | |    ||  |   | |||   | |||  || | |   | |  | ||  | |||  |   |||
    CATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAA
           140       150       160       170       180       190       200

          220       230       240       250       260       270       280
    AACAGCAGCTGGCAAGAGTAGGTCGGCTGTTCGTCGTATTCTTTGATCTGGATGGTGTTGTAGAGTTCGTCG
    ||  | || |  |  ||  |   |         |||||| |     | || | |      |    | |  |
    AATCGAAGTTATCCTGAAGAATGC-------TATCGTATACAACTCTATGTACGAAAACTT---CTCCACCT
         210       220              230       240       250          260

        290       300       310       320       330       340       350
    GAATCAGAGATCGGAGCCAGGAAAAGCTTTTCTTCTTCTTTCTTGAAGTACTTGTAGGTGTATACACGCCAT
       || |    || | || | || |  |   || | ||| |||  |            || |||||| |
    CCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAA---------CAATGAATACAC-CATC
       270       280       290       300       310                320

      360       370       380       390       400       410
    TCCTGATTCAGGTTGAAGAAGTCCAGGTAGATGTAGTCTTCTTTACGTACGATGTCATCAT--------TGA
      |   | || |   || || ||  | | ||   ||| |   | |  |||| ||  |||||        ||
    ATCAACTGCATGGAAAACAATTCTGGTTGGA--AAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGC
     330       340       350         360       370       380       390

  420          430       440       450       460       470       480
    TGGAC---TGAGAGTTAGATTTGCGACGGATGATGAACTTTTCACCGATGTACAGGTCGCGGTAGTTGATGT
     ||||      ||  |  |   |||     |  || |  || | ||||  ||         | |  ||
    AGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCA
     400       410       420       430       440       450       460

   490         500       510         520       530       540       550
    AT--TTAGAGTTCTGGTTGTATTTGGAACGA--GTCAGGATTTCACCAACCGGAGAGTCTTTCTTCAGTTTG
    ||   | ||  |  | |   ||    ||| |  ||| | ||  | ||||        ||   |  | || ||
    ATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATC-AACGGCCGTCTG
   470       480       490       500       510       520        530

      560       570       580       590       600       610       620
    ATGTAAGAGTTCTTGTTACCAGCATTGAACATATAGTATTCTTTGTTGTACATCAGCGGATTACCCCAGAAG
    ||  |  ||     | |  |     ||   |      |  |||      ||||||       ||   |
    ATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGT
  540       550       560       570       580       590       600       610

   630       640       650       660            670       680       690
    TCTTTCAGGTATTCGGAGTAAGACTGGATCTTGTAC----CGTTCTTCGATATTGGACTGAGACAGTTCGGT
    | |        |      ||    |||||||   |||       | ||||| |  | |||||   |    |
    TGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAA
          620       630       640       650       660       670       680

     700            710        720       730       740          750
    GTTGAAGA-----TGGAGAAGTATTTC-ATCCAGATGAACTGGGTACGATC---GATGTCACCGTCCAGTTT
     |  ||||       || ||  | | | || | | |   |||       ||   | || |  | | ||||
    ATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTAC
        690       700       710       720       730       740       750

  760          770       780       790       800       810       820
    G---AAGATGATTTCACCGTTAGCGATAACTTCACGGATGTCTTTGATGTCGGTATTAGATTCCAGTTTACC
    |   ||    | | ||   | |      ||    || |   |   | || ||  |  | | |  || |  ||
    GACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCA--ACAATGTAGGTATCC
      760       770       780       790       800       810         820

   830       840       850       860       870       880       890
    GTTGATGTAGATTTTAGCATTGTTCAGGTTATT-GGTGATGGTAACGAAGAACCAGCGATTGATGTATTCAG
    |  | |  |  |    | |  || |  ||  ||  || |||   || || | | | |   |||  | |||
    GCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACC---TGAACTCTTCCC
      830       840       850       860       870       880          890

  900        910       920       930       940       950       960       970
    AG-ATGTCTTCACGGATGTTGTATTCGAAGAATACAGATTTGGTCTTACCGTTGATATCGATCAGAGTCCAG
     | |       ||  |  |  |  || |  |||||   | ||||   |  |   |||||| ||   |
    TGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTC---GCAACA
       900       910       920       930       940       950          960

           980       990      1000      1010      1020      1030      1040
    ATGATACGGTTACCGCGGATGGAGATCTTCCAACCAGAGTTATTCTTCATGCAGTTGATGATGGTGTATTCA
    |||||   ||   |    |||  |   ||   | || ||     | ||  ||     ||| |  |
    ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTG
        970       980       990      1000      1010      1020      1030

        1050      1060        1070      1080      1090      1100      1110
    TTGTGGATGTAATTCTGGATACCGTCG--TTCTTGTATTTCGGGATACGAATCCAGAAGGAAACAGAGAAGT
     ||| ||    ||  ||  | |  | |   ||  | |  | || |  |     |||   |    |  ||| |
    GTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAAT
     1040      1050      1060      1070      1080      1090      1100

        1120      1130      1140       1150      1160      1170      1180
    CCAGGAATACGGAGTTGAAGATGATGTTCTG-ATTCTGAGTAACACGGATCTTAGAGTTAGCGGAAGAGGTC
    ||| |||     ||   |  |  |     || |   ||| |     |||    |  | || ||  |  |||
    CCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTT
   1110      1120      1130      1140      1150      1160      1170

       1190      1200      1210      1220      1230      1240      1250
    AGTTTGAACTGGTTCTTGTCATTCAGTTCAACACCGTCGTATACTTCAACTTTAGCACCGTAACCAGACAGA
       | |   |    |   |||   |  ||   |   | ||    | ||||  | | ||  |   ||||  ||
    TCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAAC--TGGTACAATCGTCAGATCGA
 1180      1190      1200      1210      1220        1230      1240

     1260      1270      1280      1290      1300        1310      1320
    TCGATCAGATTGTTGTCTTTGTAACGCAGGTTCAGGATGATATTGTTCAGGA--TTTCGGAATTGTATTTGT
     || ||   | |   |||  ||  | |  |   ||         ||| | ||   || ||       |  |
    ACGTTCCTCTCGCACTCTGGGTTGCTCTTG-GGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGC
 1250      1260      1270       1280      1290      1300      1310      1320

     1330      1340
    TGGCCATCGTGAATTC
    ||     || |||  |
    TGTAACCCGGGAAAGCTT
          1330     X


3. US-09-910-186A-7' (1-1341)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =      43  Optimized Score   =    481  Significance = -0.47
Residue Identity =     42%  Matches           =    577  Mismatches   =   716
Gaps             =      79  Conservative Substitutions              =     0

            10  X     20        30        40        50        60        70
    GAATTCTTACTATTCGGTCCAACCTTCGTCTTTCGGGATGAACTGCCAATTGCAACCCAGTTTCAGGTTGTA
                 |||  |||    ||||||   |          |  | | || |              ||
                CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATA
                X       10        20        30        40        50        60

          80        90       100       110       120       130       140
    CGGTTTGCGTTTAACTTCCTTCAGGTACCATTTGGAGATGCAGAAGTAGTCTTTGTATTCTTCGAATA-CGA
    |      | |  | || |  |  |   ||| |   |  ||    |   ||||   ||  |||| || | | |
    CCTCCATCCTGAACCTGCGCTACGAATCCAAT--CACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAA
            70        80        90          100       110       120       130

        150       160          170        180       190       200       210
    TACCAGATTCGTAGAAACGGTGGAT---ACCGATCAG-ACCGATTTCGTCAGTAGATTCTTCATCTTTCTTG
     | | | |    ||  |   | |||   | |||  || | |   | |  | ||  | |||  |   |||
    CATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAA
           140       150       160       170       180       190       200

          220       230       240       250       260       270       280
    AACAGCAGCTGGCAAGAGTAGGTCGGCTGTTCGTCGTATTCTTTGATCTGGATGGTGTTGTAGAGTTCGTCG
    ||  | || |  |  ||  |   |         |||||| |     | || | |      |    | |  |
    AATCGAAGTTATCCTGAAGAATGC-------TATCGTATACAACTCTATGTACGAAAACTT---CTCCACCT
         210       220              230       240       250          260

        290       300       310       320       330       340       350
    GAATCAGAGATCGGAGCCAGGAAAAGCTTTTCTTCTTCTTTCTTGAAGTACTTGTAGGTGTATACACGCCAT
       || |    || | || | || |  |   || | ||| |||  |            || |||||| |
    CCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAA---------CAATGAATACAC-CATC
       270       280       290       300       310                320

      360       370       380       390       400       410
    TCCTGATTCAGGTTGAAGAAGTCCAGGTAGATGTAGTCTTCTTTACGTACGATGTCATCAT--------TGA
      |   | || |   || || ||  | | ||   ||| |   | |  |||| ||  |||||        ||
    ATCAACTGCATGGAAAACAATTCTGGTTGGA--AAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGC
     330       340       350         360       370       380       390

  420          430       440       450       460       470       480
    TGGAC---TGAGAGTTAGATTTGCGACGGATGATGAACTTTTCACCGATGTACAGGTCGCGGTAGTTGATGT
     ||||      ||  |  |   |||     |  | || |  || | ||||  ||         | |  ||
    AGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCA
     400       410       420       430       440       450       460

   490         500       510         520       530       540       550
    AT--TTAGAGTTCTGGTTGTATTTGGAACGA--GTCAGGATTTCACCAACCGGAGAGTCTTTCTTCAGTTTG
    ||   | ||  |  | |   ||    ||| |  ||| | ||  | ||||        ||   |  | || ||
    ATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATC-AACGGCCGTCTG
   470       480       490       500       510       520        530

     560       570       580       590       600       610       620
    ATGTAAGAGTTCTTGTTACCAGCATTGAACATATAGTATTCTTTGTTGTACATCAGCGGATTACCCCAGAAG
    ||  |  ||     | |  |     ||   |      |  |||      ||||||       ||   |
    ATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGT
  540       550       560       570       580       590       600       610

   630       640       650       660           670       680       690
    TCTTTCAGGTATTCGGAGTAAGACTGGATCTTGTAC----CGTTCTTCGATATTGGACTGAGACAGTTCGGT
    | |        |      ||   |||||||   |||       | ||||| |  | |||||   |    |
    TGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAA
          620       630       640       650       660       670       680

     700            710        720       730       740          750
    GTTGAAGA-----TGGAGAAGTATTTC-ATCCAGATGAACTGGGTACGATC---GATGTCACCGTCCAGTTT
     |  ||||       || ||  | | | || | | |   |||       ||   | || |  | | ||||
    ATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTAC
        690       700       710       720       730       740       750

  760          770       780       790       800       810       820
    G---AAGATGATTTCACCGTTAGCGATAACTTCACGGATGTCTTTGATGTCGGTATTAGATTCCAGTTTACC
    |   ||    | | ||   | |      ||    || |    |  | || ||  |  | | |  || |  ||
    GACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCA--ACAATGTAGGTATCC
      760       770       780       790       800       810         820

   830       840       850       860        870       880       890
    GTTGATGTAGATTTTAGCATTGTTCAGGTTATT-GGTGATGGTAACGAAGAACCAGCGATTGATGTATTCAG
    |  | |  |  |    | |  || |  ||  ||  || |||   || || | | | |   |||  | |||
    GCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACC---TGAACTCTTCCC
      830       840       850       860       870       880          890

  900        910       920       930       940       950       960       970
    AG-ATGTCTTCACGGATGTTGTATTCGAAGAATACAGATTTGGTCTTACCGTTGATATCGATCAGAGTCCAG
     | |       ||  |  |  |  || |  |||||   | ||||   |  |   |||||| ||   |
    TGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTC---GCAACA
       900       910       920       930       940       950          960

           980       990      1000      1010      1020      1030      1040
    ATGATACGGTTACCGCGGATGGAGATCTTCCAACCAGAGTTATTCTTCATGCAGTTGATGATGGTGTATTCA
    |||||   ||   |    |||  |   ||   | || ||     | ||  ||     ||| |  |
    ATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTG
        970       980       990      1000      1010      1020      1030

        1050      1060        1070      1080      1090      1100      1110
    TTGTGGATGTAATTCTGGATACCGTCG--TTCTTGTATTTCGGGATACGAATCCAGAAGGAAACAGAGAAGT
    ||| ||    ||  ||  | |  | |   ||  | |  | || |  |     |||   |    |  ||| |
   GTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAAT
    1040      1050      1060      1070      1080      1090      1100

       1120      1130      1140       1150      1160      1170      1180
   CCAGGAATACGGAGTTGAAGATGATGTTCTG-ATTCTGAGTAACACGGATCTTAGAGTTAGCGGAAGAGGTC
   ||| |||     ||   |  |  |     || |   ||| |     |||    |  | || ||  |  |||
   CCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTT
  1110      1120      1130      1140      1150      1160      1170

      1190      1200      1210      1220      1230      1240      1250
   AGTTTGAACTGGTTCTTGTCATTCAGTTCAACACCGTCGTATACTTCAACTTTAGCACCGTAACCAGACAGA
      | |   |    |   |||   |  ||   |   | ||    | ||||  | | ||  |   ||||  ||
   TCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAAC--TGGTACAATCGTCAGATCGA
1180      1190      1200      1210      1220        1230      1240

    1260      1270      1280      1290      1300        1310      1320
   TCGATCAGATTGTTGTCTTTGTAACGCAGGTTCAGGATGATATTGTTCAGGA--TTTCGGAATTGTATTTGT
    || ||   | |   |||  ||  | |  |   ||         ||| | ||   || ||       |  |
   ACGTTCCTCTCGCACTCTGGGTTGCTCTTG-GGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGC
1250      1260      1270       1280      1290      1300      1310      1320

    1330      1340
   TGGCCATCGTGAATTC
   ||     || |||  |
   TGTAACCCGGGAAAGCTT
         1330     X
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-8.res made by bobryen on Thu 7 Nov 102 14:32:54-PST.


Query sequence being compared:US-09-910-186A-8 (1-440)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-8 (1-440) with:
        File : US08123975A.pep

   100-
       -
N      -
U   50-
M      -
B      -
E      -
R      -
       -
O      -
F   10-
       -
S      -
E    5-
Q      -
U      -
E      -
N      -
C      -
E      -                           *                                    *
S     0-----------------------------------------------------------------------
       |      |      |       |      |      |      |      |      |       |
SCORE  0      49     98     146    195    244    293    341    390     439
STDEV                        -1                   0

                              PARAMETERS

Similarity matrix       PAM-150    K-tuple                        1
Threshold level of sim.     16%
Mismatch penalty              1    Joining penalty               20
Gap penalty                5.00    Window size                  440
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                              SEARCH STATISTICS

Scores:                   Mean       Median      Standard Deviation
                          355          190        144.05

Times:                    CPU                     Total Elapsed
                      00:00:00.00                 00:00:00.00

Number of residues:                  1704
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name     Description                     Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
   1. US-08-123-975A-2 Sequence 2, Application U     850    439    439   0.58    0
   2. US-08-123-975A-5 Sequence 5, Application U     439    438    438   0.58    0
                    ****  1 standard deviation below mean ****
   3. US-08-123-975A-3 Sequence 3, Application U     415    189    259  -1.15    0


1. US-09-910-186A-8 (1-440)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    439  Optimized Score  =    439  Significance =  0.58
Residue Identity =    99%  Matches          =    438  Mismatches   =     2
Gaps             =      0  Conservative Substitutions             =     0

                        X       10        20        30        40        50
                        MANKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTS
                        | ||||||||||||||||||||||||||||||||||||||||||||||||||
    LKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTS
           400       410       420       430       440       450       460

          60        70        80        90       100       110       120
    SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTL
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTL
         470       480       490       500       510       520       530

       130       140       150       160       170       180       190
    IDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    IDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
       540       550       560       570       580       590       600

     200       210       220       230       240       250       260
    IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
     610       620       630       640       650       660       670

   270       280       290       300       310       320       330       340
    EILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEE
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    EILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEE
   680       690       700       710       720       730       740       750

            350       360       370       380       390       400       410
    KLFLAPISDSDELYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWY
    |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    KLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWY
            760       770       780       790       800       810       820

          420       430        X
    LKEVKRKPYNLKLGCNWQFIPKDEGWTE
    ||||||||||||||||||||||||||||
    LKEVKRKPYNLKLGCNWQFIPKDEGWTE
          830       840       850


2. US-09-910-186A-8 (1-440)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    438  Optimized Score  =    438  Significance =  0.58
Residue Identity =    99%  Matches          =    437  Mismatches   =     2
Gaps             =      0  Conservative Substitutions             =     0

     X      10        20        30        40        50        60        70
    MANKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVF
     X       10        20        30        40        50        60        70
```

```
          80        90       100       110       120       130       140
    LDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    LDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDI
           80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    SEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELS
        150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDL
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    QSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDL
      220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    YIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDELYNTIQIK
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
    YIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIK
    290       300       310       320       330       340       350

           370       380       390       400       410       420       430
    EYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFI
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    EYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFI
  360       370       380       390       400       410       420       430

         440
    PKDEGWTE
    ||||||||
    PKDEGWTE
           X


3. US-09-910-186A-8 (1-440)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    189  Optimized Score =     259  Significance = -1.15
Residue Identity =    38%  Matches         =     162  Mismatches   =   221
Gaps             =     17  Conservative Substitutions              =    26

            10        20        30        40          50        60        70
    MANKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELN--DKNQFKLTSSANSKIRVTQNQNIIFNS
                     ||  | ||||| |::|: :   |     ||||  |     ||| |     |::||
                     RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNS
                     X       10        20        30        40        50

            80        90       100       110       120       130       140
    VFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIRE
     :  || ||||||||| |        ||||||||| ||||||:|     ||||| |       | | |
    MYENFSTSFWIRIPKYFNSIS---LNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
        60       70            80       90       100       110       120

         150        160       170       180       190       200       210
    DISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNT
     ||:||||| ||||||| |||:||||||:|     |     : |   | |||||  |   :|| |||  |
    NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
       130       140       150       160       170       180       190

        220       230       240       250       260       270       280
    ELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINY
    ||    | : |  || |  ||||||  | | | ||| |    | |:        |    :           |
    ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
     200       210       220       230       240       250       260

      290       300       310       320       330       340       350
    RDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDELYNTI
                 |  :    | |||  | :|      | | |  |       |  |    | |   |   :
    LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
   270       280       290       300       310       320       330       340

    360       370       380       390       400       410       420
    QIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNW
      |   :|            :    :|| || | |   :            | || : : |      ||| |
    VMKSKNDQGI-TNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVA--------SNWYNRQIERS--SRTLGCSW
           350        360       370       380               390         400

  430       440
    QFIPKDEGWTE
     ||| |:|| |
    EFIPVDDGWGERPL
          410 X
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9.res made by bobryen on Thu 7 Nov 102 14:42:59-PST.


Query sequence being compared:US-09-910-186A-9 (1-1371)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-9 (1-1371) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                           *
N     -
C     -
E     -                                                           *
S    0------------------------------------------------------------------
      |      |     |  |   |     ||     | |    |    | |     | |    |
SCORE 0     37    74  | 110    147   184 |  221    257   294 |  331
STDEV       -4       -3        -2       -1         0         1


                              PARAMETERS

Similarity matrix        Unitary     K-tuple                     4
Mismatch penalty               1     Joining penalty            30
Gap penalty                 5.00     Window size               500
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                            SEARCH STATISTICS

Scores:                  Mean        Median       Standard Deviation
                         270          241           52.54

Times:                   CPU                      Total Elapsed
                     00:00:00.00                 00:00:01.00

Number of residues:                   4027
Number of sequences searched:            3
Number of scores above cutoff:           3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
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                                                          Init.  Opt.
Sequence Name      Description                    Length Score  Score  Sig. Frame
---------------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351    331    618   1.16   0
                  ****  0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338    240    620  -0.57   0
  3. US-08-123-975A-1 Sequence 1, Application U   1338    240    620  -0.57   0


1. US-09-910-186A-9 (1-1371)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    331  Optimized Score  =    618  Significance =  1.16
Residue Identity  =    50%  Matches          =    706  Mismatches   =   545
Gaps              =    138  Conservative Substitutions              =     0

     40        50        60        70        80        90       100
   ACACCAACAACTCCCTGTTGAAGGACATCATCAACGAGTACTTCAACAACATCAACGACTCCAAGATCCTGT
                       | ||   ||| |||  |  | | | | | | | ||| |    |  ||||||
                       ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAA---TATCATCCTGA
                       X        10        20        30           40

  110       120       130       140       150       160       170       180
   CCCTGCAGAACCGTAAGAACACCTTGGTCGACACCTCCGGTTACAACGCCGAGGTCTCCGAGGAGGGTGACG
    |||||   ||    | ||||   || ||||    || ||||||   ||  | ||    |   | |  |  |
   ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTG
   50        60        70        80        90       100       110       120

          190       200       210       220       230       240       250
   TCCAGCTGAACCCAATCTTCCCATTCGACTTCAAGCTGGGTTCCTCCGGTGAGGACAGAGGTAAGGTCATCG
   |  | |||||    |    ||      | ||||| |||   || |||| |      |    |||| ||   |
   TTGAACTGAATGACAAGAACC------AGTTCAAACTGACCTCTTCCGCT------AACTCTAAGATCCGTG
          130       140             150       160             170       180

        260       270       280       290       300       310       320
   TCACCCAGAACGAGAACATCGTCTACAACTCCATGTACGAGTCCTTCTCCATCTCCTTCTGGATCAGAATC-
   | || |||||  |||||||| ||| ||||||| | | |  |  ||||||  | |||||||||||| | |||
   TTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCC
          190       200       210       220       230       240       250

                330       340               350       360       370
   ---------AACAAGTGGGTCTCCAACTTGCCA--------GGTTACACCATCATCGACTCCGTCAAGAACA
            |  | |  ||| ||||   |  ||        |  |||||||||||| ||| | | ||||| |
   CGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATA
        260       270       280       290       300       310       320

  380       390       400       410       420       430       440       450
   ACTCCGGTTGGTCCATCGGTATCATCTCCAACTTCCTGGTCTTCACCCTGAAGCAGAACGAGGACTCCGAGC
   |||| ||||||   |||   |||  |   |||    |  |||  || ||||   | | | | |
   ACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCA
      330       340       350       360       370       380       390

          460       470       480       490       500          510      520
   AGTCCATCAACTTCTCCTACGACATCTCCAACAACGCTCCTGGTTACAACAA---GTGGTTCTTCGTCACCG
   | ||  |   ||||   ||| |||||    |  ||    |||  |||| |||    ||||||||||| |||
   AATCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCA
   400       410       420       430       440       450       460

           530       540       550       560       570       580       590
   TCACCAACAACATGATGGGTAACATGAAGATCTACATCAACGGTAAGCTGATCGACACCATCAAGGTCAAGG
   ||||||| ||| |||     ||    || ||||||||||||||||| |||      |  | | |  |||| |
   TCACCAATAACCTGA---ACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAG
 470        480          490       500       510       520       530

         600       610       620       630       640       650       660
   AGTTGACCGGTATCAACTTCTCCAAGACCATCACCTTCGAGATCAACAAGATCCCAGACACCGGTCTGATCA
   |  |    |   | | |     |      |||| ||      ||||   |  |   |||| || ||  | |
   ACATCCGTGAAGTTATCGCTAACGGTGAAATCATCT------TCAAACTGGACGGTGACATCGATCGTACCC
   540       550       560       570             580       590       600

       670       680       690       700       710       720       730
   CCTCCGACTCCGACAACATCAACATGTGGATCCGTGACTTCTACATCTTCGCCAAGGAGTTGGACGGTAAGG
  |                   ||| |||||     |||||| |||||||  ||  ||  ||
  AGT------------------TCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCA
                       610       620       630       640       650

   740       750       760       770       780       790       800
  ACATCAACATCCTGTTCAACTCCTTGCAGTACACCAACGTCGTCAAGGACTACTGGGGTAACGACCTGAGAT
  | ||| |    | || |||   |  |   ||| || |   | | || ||||||||||||||    ||||  |
  ATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGT
 660       670       680       690       700       710       720       730

 810       820       830       840       850
  ACAACAAGGAGTACTACATGGTCAACATCGACTACTTGAACAGATACAT----------------------G
  ||||||| || ||||| ||| ||||    |   ||  ||||   |||||                      |
  ACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGG
         740       750       760       770       780       790       800

 860       870       880       890                  900       910
  TACGCCAACTCCAGACAGATCGTCTTCAACACCAGACGT-----------AACAACAACGACTTCAACGAGG
  |  |  || ||| |||   |       |  ||||||  |           ||| ||  |||| |  ||   |
  TTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCG
       810       820       830       840       850       860       870

920       930       940       950       960       970       980       990
  GTTACAAGATCATCATCAAGCGTATCAGAGGTAACACCAACGACACCAGAGTCAGAGGTGGTGACATCCTGT
  || | ||| ||||||||   |||  || |  |||| |  |   || ||          || |||||||  ||
  GTGAAAAGTTCATCATC---CGTCGCAAATCTAACTCTCAGTCCATCA---------ATGATGACATC--GT
     880       890         900       910               920       930

       1000      1010      1020      1030      1040      1050      1060
  ACTTCGACATGACTATCAACAACAAGGCCTACAACCTGTTCATGAAGAACGAGACCATGTACGCCGACAACC
  || |  | | ||||| || | ||  || || |  |    | |   || |   |    | ||| || ||||
  ACGTAAAGAAGACTA-CATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGT
       940       950       960       970       980       990       1000

     1070      1080      1090      1100      1110      1120      1130
  ACTCCACCGAGGACATCTACGCCATCGGTCTGCGTGAGCAGACCAAGGACATCAACGACAACATCATCTTCC
  ||| ||   | ||     |     |    |||  |  |    |  |   |  | |   | ||| || | |||
  ACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCC
     1010      1020      1030      1040      1050      1060      1070

   1140      1150      1160      1170      1180      1190      1200
  AGATCCAGCCAATGAACAACACTTACTACTACGCTTCCCAGATCTTCAAGTCCAACTTCAACGGTGAGAACA
  ||||| |   |    || |         |||| ||| |||| |  |   || |||     | |  ||    |
  AGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCT---GTTCAAGAAAGATGAAGAATCTA
   1080      1090      1100      1110      1120       1130      1140

 1210      1220      1230      1240               1250      1260      1270
  TCTCCGGTATCTGTTCCATCGGTACCTACAGATTC---------CGTCTGGGTGGTGACTGGTACAGACACA
      ||  ||| ||   ||||||| | || | |||          || | |     ||    |||| | ||
  CTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACT
    1150      1160      1170      1180      1190      1200      1210

        1280            1290      1300         1310      1320      1330
  ACTACTTGGT-TCCAACTG-----TCAAGCAGGGTAA---CTACGCCTCCTTGCTGGAGTCCACTTCCACCC
  ||| ||   | ||||| ||     | ||| | | |||   | |  | | |   ||| |      || ||
  ACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTGCA---
  1220      1230      1240      1250      1260      1270      1280

     1340         1350      1360          X
  ACTGGGGATTCGTCCC---AGTCTCCGAGTAATAGGAATTC
  | |||   ||| ||||   || |   |  |     ||||
  ATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCC
   1290      1300      1310      1320      1330      1340


2. US-09-910-186A-9 (1-1371)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    240  Optimized Score  =    620  Significance = -0.57
Residue Identity  =    49%  Matches          =    686  Mismatches   =   593
Gaps              =    111  Conservative Substitutions              =     0

  20        30        40        50        60        70        80
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  CCATTCAACATCTTCTCCTACACCAACAACTCCCTGT-TGAAGGACATCATCAACGAGTACTTCAACAACAT
                      | | | | |   |  || ||  |   | | |||  || ||| |||| |||||
                      CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                      X       10        20        30        40        50

 90      100       110       120       130       140       150       160
  CAACGACTCCAAGATCCTGTCCCTGCAGAACCGTAAGAACACCTTGGTCGACACCTCCGGTTACAACGCCGA
  || | |  ||   ||||||  |||||   ||      ||   | || |||||   ||  | |||    || |
  CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
        60        70        80        90       100       110       120

        170       180       190       200       210       220       230
  GGTCTCCGAGGAGGGTGACGTCCAGCTGAACCCAATCTTCCCATTCGACTTCAAGCTGGGTTCCTCCGGTGA
    ||  |   |    | | ||  |  |  | || |||  |       |  || |||||      | |  |
  AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTG------TTCAATCT
     130       140       150       160       170       180             190

      240       250       260       270       280       290       300
  GGACAGAGGTAAGGTCATCGTCACCCAGAACGAGAACATCGTCTACAACTCCATGTACGAGTCCTTCTCCAT
  |||       ||  ||   || | || |||  |    ||||| |||||||| ||||||||   ||||||||
  GGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCAC
         200       210       220       230       240       250       260

    310       320          330       340             350       360
  CTCCTTCTGGATCAGAATC---AACAAGTGGGTCTCCAACTTGC------CAGGTTACACCATCATCGACTC
  ||||||||||||| | |||   ||  | |    ||||| ||  |        |  |||||||||||| |||
  CTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTG
       270       280       290       300       310       320       330

 370       380       390       400       410       420       430       440
  CGTCAAGAACAACTCCGGTTGGTCCATCGGTATCATCTCCAACTTCCTGGTCTTCACCCTGAAGCAGAACGA
  | |  | ||||| || ||||||    |   | | | || |       |  |||  || ||| || | |   |
  CATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCA
     340       350       360       370       380       390       400

         450       460       470       480       490       500
  GGACTCCGAGCAGTCCATCAACTTCTCCTACGACATCTCCAACAACGCTCCTGGTTACAACAA---GTGGTT
  |||   | | |||    |    |||   |||         | ||||    |||  |||| |||    ||| |
  GGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGAT
   410       420       430       440       450       460       470

510       520       530       540       550       560       570       580
  CTTCGTCACCGTCACCAACAACATGATGGGTAACATGAAGATCTACATCAACGGTAAGCTGATCGACACCAT
  |||||| ||| ||||||||||     ||  ||||   || ||||||||||||||    |||||||||   |
  CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAA
 480       490       500       510       520       530       540       550

        590       600       610       620       630       640       650
  CAAGGTCAAGGAGTTGACCGGTATCAACTTCTCCAAGACCATCACCTTCGAGATCAACAAGATCCCAGACAC
     | ||    |  ||      ||| ||   || || | |||||  |||                   | ||
  ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTC-------------------AAAC
         560       570       580       590                          600

      660       670       680       690       700       710       720
  CGGTCTGATCACCTCCGACTCCGACAACATCAACATGTGGATCCGTGACTTCTACATCTTCGCCAAGGAGTT
   || | | |  | |   ||||     ||  | |||| ||||||    ||||| |  | |||| ||| ||  |
  TGGACGGTTGTCGTGACACTC-----ACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACT
      610       620            630       640       650       660       670

    730       740       750       760       770       780       790
  GGACGGTAAGGACATCAACATCCTGTTCAACTCCTTGCAGTACACCAACGTCGTCAAGGACTACTGGGGTAA
  | |||  || || |||||   ||||| | ||  |  |    |  |     || | || |||| ||||||| |
  GAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGA
         680       690       700       710       720       730       740

  800       810       820       830       840       850       860
  CGACCTGAGATACAACAAGGAGTACTACATGGTCAACATCGACTACTTGAACAGATACATGTACGCCAACTC
  | |||||   ||| ||||   |||||||||| | ||  |  || |   ||||| |||| |  ||| ||||
  CTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAA
       750       760       770       780       790       800       810

870       880           890                              900       910
  CAGACAGATCGTCTTCAAC----ACCAGA-----------------------CGTAACAACAACGACTTCA-
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        |   |||  |    ||    ||| ||                         || ||||| | || | |
     TGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAA
             820       830       840       850       860       870       880

                        920       930       940       950       960       970
     -----------ACGAGGGTTACAAGATCATCATCAAGCGTATCAGAGGTAACACCAACGACACCAGAGTCAG
                ||   |||  |||  |||||||||||     |     |   | ||| ||||  |  ||  |
     CTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCG
           890       900       910       920       930       940       950

             980       990      1000      1010      1020      1030         1040
     AGGTGGTGACATCCTGTACTTCGACATGACTATCAACAACAAGGCCTACAACCTGTTCATGAA---GAACGA
           |||     | ||| || |  |     | || ||||| |  |||   |||   |  ||        |
     CAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA
         960       970       980       990      1000      1010      1020      1030

             1050      1060      1070      1080      1090      1100      1110
     GACCATGTACGCCGACAACCACTCCACCGAGGACATCTACGCCATCGGTCTGCGTGAGCAGACCAAGGACAT
     | |       |   | | |   ||  |   ||| |||   | | | |||   |     |||      |  ||
     GGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAAT
                1040      1050      1060      1070      1080      1090      1100

           1120      1130      1140      1150      1160      1170      1180
     CAACGACAACATCATCTTCCAGATCCAGCCAATGAACAACACTTACTACTACGCTTCCCAGATCTTCAAGTC
      ||   ||| |         |   ||||   || |  ||||  | | |      |   |||  |  |||
     GAAATCCAAGA---------ACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
              1110               1120      1130      1140      1150      1160

         1190      1200      1210      1220      1230      1240      1250
     CAACTTCAACGGTGAGAACATCTCCGGTATCTGTTCCATCGGTACCTACAGATTCCGTCTGGGTGGTGACTG
      |||   | ||||       ||  |||| ||       ||   |    |      |   | | |    ||||
     TAACGATATCGGT------TTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTG
           1170            1180      1190      1200      1210      1220      1230

       1260      1270      1280      1290      1300      1310      1320      1330
     GTACAGACACAACTACTTGGTTCCAACTGTCAAGCAGGGTAACTACGCCTCCTTGCTGGAGTCCACTTCCAC
     |||||  |   |   |     | |  ||  ||  | ||||  ||       ||||  ||||| ||   |
     GTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCT-------CTTG--GGAGTTCATCCCGGT
               1240      1250      1260      1270               1280      1290

               1340      1350      1360        1370
     CCACTGGGGATTCGTCCCAGTCTCCGAGTAA--TAGGAATTC
       |    || |  |    |    |   ||||    ||||  |
     TGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
            1300      1310      1320      1330     X


3. US-09-910-186A-9 (1-1371)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    240  Optimized Score      =    620  Significance = -0.57
Residue Identity  =    49%  Matches              =    686  Mismatches   =   593
Gaps              =    111  Conservative Substitutions                   =     0

     20        30        40        50        60        70        80
     CCATTCAACATCTTCTCCTACACCAACAACTCCCTGT-TGAAGGACATCATCAACGAGTACTTCAACAACAT
                         | | | | |   |  || ||  |   | | |||  || ||| |||| |||||
                         CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                         X       10        20        30        40        50

    90       100       110       120       130       140       150       160
     CAACGACTCCAAGATCCTGTCCCTGCAGAACCGTAAGAACACCTTGGTCGACACCTCCGGTTACAACGCCGA
     || | |  ||   ||||||  |||||   ||      ||   | || |||||   ||  | |||    || |
     CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
            60        70        80        90       100       110       120

           170       180       190       200       210       220       230
     GGTCTCCGAGGAGGGTGACGTCCAGCTGAACCCAATCTTCCCATTCGACTTCAAGCTGGGTTCCTCCGGTGA
       ||  |   |    | | ||  |  |  | || |||  |       |  || |||||      | |  |
     AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTG------TTCAATCT
         130       140       150       160       170       180             190

          240       250       260       270       280       290       300
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     GGACAGAGGTAAGGTCATCGTCACCCAGAACGAGAACATCGTCTACAACTCCATGTACGAGTCCTTCTCCAT
     |||       ||  ||   || | || |||  |    ||||| |||||||| ||||||||   ||||||||
     GGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCAC
                 200       210       220       230       240       250       260

        310       320          330       340             350       360
     CTCCTTCTGGATCAGAATC---AACAAGTGGGTCTCCAACTTGC------CAGGTTACACCATCATCGACTC
     ||||||||||||| | |||   ||  | |    ||||| ||  |        |  |||||||||||| |||
     CTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTG
               270       280       290       300       310       320       330

    370       380       390       400       410       420       430       440
     CGTCAAGAACAACTCCGGTTGGTCCATCGGTATCATCTCCAACTTCCTGGTCTTCACCCTGAAGCAGAACGA
     | |  | ||||| || ||||||    |   | | | || |       |  |||  || ||| || | |   |
     CATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCA
             340       350       360       370       380       390       400

                 450       460       470       480       490       500
     GGACTCCGAGCAGTCCATCAACTTCTCCTACGACATCTCCAACAACGCTCCTGGTTACAACAA---GTGGTT
     |||   | | |||    |    |||   |||         | ||||    |||  |||| |||    ||| |
     GGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGAT
           410       420       430       440       450       460       470

   510       520       530       540       550       560       570       580
     CTTCGTCACCGTCACCAACAACATGATGGGTAACATGAAGATCTACATCAACGGTAAGCTGATCGACACCAT
     |||||| ||| ||||||||||     ||  ||||   || ||||||||||||||    |||||||||   |
     CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAA
    480       490       500       510       520       530       540       550

            590       600       610       620       630       640       650
     CAAGGTCAAGGAGTTGACCGGTATCAACTTCTCCAAGACCATCACCTTCGAGATCAACAAGATCCCAGACAC
        | ||    |  ||      ||| ||   || || | |||||  |||                   | ||
     ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTC-------------------AAAC
                 560       570       580       590                          600

          660       670       680       690       700       710       720
     CGGTCTGATCACCTCCGACTCCGACAACATCAACATGTGGATCCGTGACTTCTACATCTTCGCCAAGGAGTT
      || | | |  | |   ||||     ||  | |||| ||||||    ||||| |  | |||| ||| ||  |
     TGGACGGTTGTCGTGACACTC-----ACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACT
          610       620            630       640       650       660       670

        730       740       750       760       770       780       790
     GGACGGTAAGGACATCAACATCCTGTTCAACTCCTTGCAGTACACCAACGTCGTCAAGGACTACTGGGGTAA
     | |||  || || |||||   ||||| | ||  |  |    |  |     || | || |||| ||||||| |
     GAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGA
                 680       690       700       710       720       730       740

      800       810       820       830       840       850       860
     CGACCTGAGATACAACAAGGAGTACTACATGGTCAACATCGACTACTTGAACAGATACATGTACGCCAACTC
     | |||||   ||| ||||   |||||||||| | ||  |  || |   ||||| |||| |  ||| ||||
     CTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAA
               750       760       770       780       790       800       810

   870       880           890                              900       910
     CAGACAGATCGTCTTCAAC----ACCAGA-----------------------CGTAACAACAACGACTTCA-
        |   |||  |    ||    ||| ||                         || ||||| | || | |
     TGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAA
             820       830       840       850       860       870       880

                        920       930       940       950       960       970
     -----------ACGAGGGTTACAAGATCATCATCAAGCGTATCAGAGGTAACACCAACGACACCAGAGTCAG
                ||   |||  |||  |||||||||||     |     |   | ||| ||||  |  ||  |
     CTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCG
           890       900       910       920       930       940       950

             980       990      1000      1010      1020      1030         1040
     AGGTGGTGACATCCTGTACTTCGACATGACTATCAACAACAAGGCCTACAACCTGTTCATGAA---GAACGA
           |||     | ||| || |  |     | || ||||| |  |||   |||   |  ||        |
     CAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA
         960       970       980       990      1000      1010      1020      1030

             1050      1060      1070      1080      1090      1100      1110
     GACCATGTACGCCGACAACCACTCCACCGAGGACATCTACGCCATCGGTCTGCGTGAGCAGACCAAGGACAT
   | |       |   | | |   ||  |   ||| |||   | | | |||   |     |||      |  ||
   GGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAAT
         1040      1050      1060      1070      1080      1090      1100

    1120      1130      1140      1150      1160      1170      1180
   CAACGACAACATCATCTTCCAGATCCAGCCAATGAACAACACTTACTACTACGCTTCCCAGATCTTCAAGTC
    ||   ||| |         |   ||||   || |  ||||  | | |      |   |||  |  |||
   GAAATCCAAGA---------ACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGG
       1110               1120      1130      1140      1150      1160

  1190      1200      1210      1220      1230      1240      1250
   CAACTTCAACGGTGAGAACATCTCCGGTATCTGTTCCATCGGTACCTACAGATTCCGTCTGGGTGGTGACTG
    |||   | ||||       ||  |||| ||       ||   |    |      |   | | |    ||||
   TAACGATATCGGT------TTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTG
    1170            1180      1190      1200      1210      1220      1230

1260      1270      1280      1290      1300      1310      1320      1330
   GTACAGACACAACTACTTGGTTCCAACTGTCAAGCAGGGTAACTACGCCTCCTTGCTGGAGTCCACTTCCAC
   |||||  |   |   |     | |  ||  ||  | ||||  ||       ||||  ||||| ||   |
   GTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCT-------CTTG--GGAGTTCATCCCGGT
        1240      1250      1260      1270               1280      1290

        1340      1350      1360        1370
   CCACTGGGGATTCGTCCCAGTCTCCGAGTAA--TAGGAATTC
     |    || |  |    |    |   ||||    ||||  |
   TGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
     1300      1310      1320      1330     X
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> O <
O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-9-inv.res made by bobryen on Thu 7 Nov 102 14:43:14-PST.


Query sequence being compared:US-09-910-186A-9' (1-1371)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-9' (1-1371) with:
        File : US08123975A.seq

 100-
      -
N     -
U  50-
M     -
B     -
E     -
R     -
      -
O     -
F  10-
      -
S     -
E   5-
Q     -
U     -
E     -                                              *
N     -
C     -
E     -                                                                  *
S   0-----------------------------------------------------------------------
       |   |  |      |      |    |  |      ||     |    |  |      ||     |
SCORE 0   |  6     12     19    | 25    31|     37    | 44     50|     56
STDEV     -4        -3          -2         -1          0           1

                          PARAMETERS

Similarity matrix       Unitary    K-tuple                  4
Mismatch penalty              1    Joining penalty         30
Gap penalty                5.00    Window size            500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                             45           41            9.24

Times:                      CPU                  Total Elapsed
                      00:00:00.00                00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

complement

```
                                                          Init. Opt.
Sequence Name     Description                     Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                      ****  1 standard deviation above mean ****
   1. US-08-123-975A-6 Sequence 6, Application U   1351    56   435   1.19   0
                      ****  0 standard deviation from mean ****
   2. US-08-123-975A-4 Sequence 4, Application U   1338    40   404  -0.54   0
   3. US-08-123-975A-1 Sequence 1, Application U   1338    40   404  -0.54   0


1. US-09-910-186A-9' (1-1371)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =     56  Optimized Score  =    435  Significance =  1.19
Residue Identity  =    41%  Matches          =    539  Mismatches   =   670
Gaps              =    104  Conservative Substitutions              =     0

         100       110  X    120       130       140       150       160
    CCAAGTAGTTGTGTCTGTACCAGTCACCACCCAGACGGAATCTGTAGGTACCGATGGAACAGATACCGGAGA
                          | |      || |   |||    |  | | ||   |    || | | |
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X       10        20        30        40        50

       170       180       190       200       210       220       230
    TGTTCTCACCGTTGAAGTTGGACTTGAAGATCTGGGAAGCGTAGTAGTAAGTGTTGTTCATTGGCTGGATCT
    ||       ||||  |     |    |  |||||   | ||   |     ||   | |  |    | ||  |
    TG-------CGTTACA----AAGACAACAATCTG---ATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGT
                 60            70           80        90       100       110

     240       250       260       270       280       290       300
    GGAAGATGATGTTGTCGTTGATGTCCTTGGTCTGCTCACGCAGACCGATGGCGTAGATGTCCTCGGTGGAGT
      | || | |||||   |  ||| |      | | |||  | ||||  |  ||   |    ||  | .  ||
    ATACGACGGTGTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAA--CTCTAAGATCCGT
           120       130       140       150       160         170       180

   310           320       330       340          350       360       370
    GGTTGTCGG----CGTACATGGTCTCGTTCTTCATGAACAGG---TTGTAGGCCTTGTTGTTGATAGTCATG
    | |  || |     | ||||  |||    || | |   |  |   || |  |  |  || | |||    ||
    GTTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATC
           190       200       210       220       230       240       250

        380       390       400       410       420       430       440
    TCGAAGTACAGGATGTCACCACCTCTGACTCTGGTGTCGTTGGTGTTACCTCTGATACGCTTGATGATGATC
     |||| |||| ||           | || |    |       |  |   |  | ||   ||  |||| ||
    CCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAAT
         260       270       280       290       300       310       320

      450       460         470        480       490       500       510
    TTGTAACCCTCGTTGAAGTCGTT--GTTGTTA-CGTCTGGTGTTGAAGACGATCTGTCTGGAGTTGGCGTAC
       |     | |  ||  ||  |  |  || | ||| |  | | ||    ||||  | |  |      |  |
    AACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACC
       330       340       350       360       370       380       390

       520       530       540       550            560       570
    ATGTATCTGTTCAAGTAGTCGATGTTGACCATGTAGTACTCCTTG-----TTGTATCTCAGG----TCGTTA
    |  | | | |||    | |  |   |  || || ||   ||  ||      |  ||| | ||    ||||||
    AAATCTGTATTCTTCGAATACAACAT--CCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTA
     400       410       420         430       440       450       460

        580       590       600       610       620       630       640
    CC----CCAGTAGTCCTTGACGACGTTGGTGTACTGCAAGGAGTTGAACAGGATGTTGATGTCCTTACCGTC
    ||    ||| ||  |||  || | | |    |          | | ||| |||   | ||  |   | |
    CCATCACCAATA-ACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAA
     470        480       490       500       510       520       530

      650       660       670       680       690       700       710
    CAACTCCTTGGCGAAGATGTAGAAGTCACGGATCCACATGTTGATGTTGTCGGAGTCGGAGGTGATCAGACC
     |  ||| |            ||||| |  | |     ||      |  ||  | | |  |||||
    GACATCCGT------------GAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGA-------
    540                   550       560       570       580       590

    720       730       740       750       760       770       780
    GGTGTCTGGGATCTTGTTGATCTCGAAGGTGATGGTCTTGGAGAAGTTGATACCGGTCAACTCCTTGACCTT
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     |   | | | |  ||| |||| ||   |||    |||    |  || |   | |  ||||   | |
   CATCGATCGTACCCAGTTCATCTGGA---TGAAATACTTCTCCATCTTCAACACCG--AACTGTCTCAGTCC
          600       610          620       630       640         650

 790       800       810       820       830       840       850
   GATGGTGTCGATCAGCTTACCGTTGATGTAGATCTTCATGTTACCCATCATGTTGTTGGTGA---CGGTGAC
    ||   |  || | | |    | |   ||    || |   |  |  |     || | ||  |   || |||
   AATATCGAAGAAC-GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGAT
   660       670        680       690       700       710       720

  860       870       880       890            900       910       920
   GAAGAACCACTTGTTGTAACCAGGAGCGTTGTTGG-----AGATGTCGTAGGAGAAGTTGATGGACTGCTCG
   | | ||| |    |  ||   | | |  ||  |||     |||  || ||    ||  ||| | |   |||
   GTACAACAAAGAATACTA--TATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCT
  730       740         750       760       770       780       790

     930       940       950       960       970       980       990
   GAGTCCTCGTTCTGCTTCAGGGTGAAGACCAGGAAGTTGGAGATGATACCGATGGACCAACCGGAGTTGTTC
     |           | | |        |     ||   | |    | |   ||  || | |  ||  ||| |
   CCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTAC
  800       810       820       830       840       850       860       870

  1000      1010      1020      1030      1040      1050      1060
   TTGACGGAGTCGATGATGGTGTAACCTGGCAAGTTGGAGACCCACTTGTTGATTCTGATCCAGAAGGAGATG
    |    ||   | | ||  |    | | |||| |   |  | || |   | | |     |         |
   ATCGGTGAAAAGTTCATCAT---CCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAA
          880       890          900       910       920       930

1070      1080      1090      1100       1110      1120      1130      1140
   GAGAAGGACTCGTACATGGAGTTGTAGACGATG-TTCTCGTTCTGGGTGACGATGACCTTACCTCTGTCCTC
   ||  |  ||   ||| |||| || |  |   ||  ||  |    | |||   |   |   |  |   ||
   GAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAG
 940       950       960       970       980       990      1000      1010

         1150      1160      1170         1180      1190      1200
   ACCGGAGGAACCCAGCTTGAAGTCGAATGG---GAAGATTGGGTTCAGCTGGACGTCACCCTCC---TCGGA
   |  | || |    |||||    | |    |      ||||  |   | ||  ||  |||| |||   ||  |
   AAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAA
        1020      1030      1040      1050      1060      1070      1080

   1210      1220      1230      1240                 1250      1260
   GACCTCGGCGTTGTAACCGGAGGTGTCGACCAAGGTGTTCTT-----------ACGGTTCTGC--AGGGACA
   ||   || ||    | |||      ||   | || || | ||           | |  ||| |  | | |
   GAATACGACG-AACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAAT
      1090       1100      1110      1120      1130      1140      1150

    1270      1280      1290      1300      1310      1320       1330
   GGATCTTGGAGTCGTTGATGTTGTTGAAGTACTCGTTGATGATGTCCTTCAACAGGGAG-TTGTTGGTGTAG
    | |||    |   |  |   | |  | | |   | |   |   ||    || |   ||  |  |  || |
   CGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCAT
     1160      1170      1180      1190      1200      1210      1220

   1340      1350        1360      1370
   GAGAAGATGTTGAATG--GGATGGTCATCGTGAATTC
       | ||| |   ||  ||| | | | ||  ||
   CTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTG
   1230      1240      1250      1260  X   1270      1280

2. US-09-910-186A-9' (1-1371)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     40  Optimized Score  =    404  Significance = -0.54
Residue Identity =    40%  Matches          =    485  Mismatches   =   626
Gaps             =     91  Conservative Substitutions              =     0

  190       200       210       220       230       240       250       260
   TGAAGATCTGGGAAGCGTAGTAGTAAGTGTTGTTCATTGGCTGGATCTGGAAGATGATGTTGTCGTTGATGT
                           |    | | || |  ||||  |        |||     ||    |  |
                       CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                       X       10        20        30        40        50

          270       280       290        300        310       320       330
   CCTTGGTCTGCTCACGCAGACCGATGGCGTAG-ATGTCCTCGGTGGAGTG-GTTGTCGGCGTACATGGTCTC
   | |   |     ||  | || |    ||   | ||    ||    ||  |   ||||    |||     |
   CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
         60        70        80        90       100       110       120

          340       350       360       370       380       390       400
   GTTCTTCATGAACAGGTTGTAGGCCTTGTTGTTGATAGTCATGTCGAAGTACAGGATGTCACCACCTCTGAC
     ||  |||               |||      ||| | || |    ||  |  | |||         | |
   AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGT---------TCAA
      130       140       150       160       170       180

        410       420       430       440       450       460       470
   TCTGGTGTCGTTGGTGTTACCTCTGATACGCTTGATGATGATCTTGTAACCCTCGTTGAAGTCGTTGTTGTT
   |||||  || |      |     | || |    ||     ||| | ||   |||  || |       || |
   TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
   190       200       210       220       230       240       250

      480       490       500       510       520       530       540
   ACGTCTGGTGTTGAAGACGATCTGTCTGGAGTTGGCGTACATGTATCTGTTCAAGTAGTCGATGTTGACCAT
           | | ||     |||       | ||    | ||| | ||||  |||  | |  |   | | ||
   CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAA
 260       270       280       290       300       310       320       330

            550       560       570       580        590       600
   GT--------AGTACTCCTTGTTGTATCTCAGGTCGTTACCCCAGT-AGTCCTTGACGACGTTGGTGTAC-T
    |        |  | | || |||| |    |  ||   ||  | || |   | |   |||  ||  | ||
   CTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACAC
         340       350       360       370       380       390       400

  610       620       630       640       650       660       670       680
   GCAAGGAGTTGAACAGGATGTTGATGTCCTTACCGTCCAACTCCTTGGCGAAGATGTAGAAGTCACGGATCC
    || | | |  |||||  |||||            | ||| | ||    || |||  | |  ||      |
   TCAGGAAATCAAACAGCGTGTTG----------TATTCAAATACTCTCAGATGATCAACATCTCTGACTACA
       410       420                 430       440       450       460

          690       700       710       720       730       740       750
   ACATGTTGATGTTGTCGGAGTCGGAGGTGATCAGACCGGTGTCTGGGATCTTGTTGATCTCGAAGGTGATGG
    ||       | | |  |   |       | ||  |   ||  |            | ||| ||  |
   TCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAAT------------AACTCCAAAATCTACA
     470       480       490       500                   510       520

        760       770       780       790       800       810       820
   TCTTGGAGAAGTTGATACCGGTCAACTCCTTGACCTTGATGGTGTCGATCAGCTTACCGTTGATGTAGATCT
   ||   |      ||||       ||  |  |  ||    |||     |||  |    |        | | |
   TCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTC------TAATAACA
     530       540       550       560       570       580             590

      830        840       850       860       870       880       890
   TCATGTT-ACCCATCATGTTGTTGGTGACGGTGACGAAGAACCACTTGTTGTAACCAGGAGCGTTGTTGGAG
   ||||||| |  |   | | |  | |||||  | ||     ||  || | |  ||          |||| ||
   TCATGTTCAAACTGGACGGTTGTCGTGACACTCAC-CGCTACATCTGGATCAAATACTTCAATCTGTTCGA-
         600       610       620        630       640       650       660

     900       910       920       930       940       950       960
   ATGTCGTAGGAGAAGTTGATGGACTGCTCGGAGTCCTCGTTCTGCTTCAGGGTGAAGACCAGGAAGTTGGAG
       |  || |      ||   |    ||  || ||| || |  |  |  |   ||  |  | |   || |
   ----CAAAGAACTGAACGAAAAAGAAATCAAAGACCT-GTACGACAACCAGTCCAATTCTGGTATCCTGAAA
             670       680       690        700       710       720

   970       980       990      1000      1010      1020      1030
   ATGATACCGATGGACCAACCGGAGTTGTTCTTGACGGAGTCGATGATGGTGTAACCTGGCAAGTTGGAGACC
       |   |   ||| | | | |||    |    || | |  ||| ||    || || | | | |    ||
   GACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTG----AATCT-GTACGATCCGAACA
  730       740       750       760       770           780        790

1040      1050      1060      1070      1080      1090      1100      1110
   CACTTGTTGATTCTGATCCAGAAGGAGATGGAGAAGGACTCGTACATGGAGTTGTAGACGATGTTCTCGTTC
    |   |||||   | | | |    |  ||        ||  |||| | ||   ||   ||  ||||| |||
   AATACGTTGA-CGTCAACAATGTAGGTATCCGCGGTTACATGTACCT-GAAAGGTCCGCGTGGTTCT-GTTA
     800        810       820       830       840        850       860

           1120      1130      1140      1150      1160      1170      1180
   TGGGT---GACGATGACCTTACCTCTGTCCTCACCGGAGGAACCCAGCTTGAAGTCGAATGGGAAGATTGGG
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    ||  |    ||    |||| | ||||  |||   | | || ||| |  |     || |     | |  |  |
    TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
       870       880       890       900       910       920       930

          1190      1200      1210      1220      1230            1240
    TTCAGCTGGACGTCACCCTCCTCGGAGACCTCGGCGTTGTAACCGGAGGTGTCG------ACCAAGGTGTTC
     | |   ||||   | | | | |    |     | ||    | |   | ||| |      || |||     |
    GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
     940       950       960       970       980       990      1000

    1250      1260         1270            1280      1290      1300
    TTACGGTTCTGCAGG---GACAGGATCTTGGAG------TCGTTGATGTTGTTGAAGTACTCGTTGATGATG
     |  || |    | |     |||| |  || ||      || |   || | | ||| | |  |  || |
    GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
  1010      1020      1030      1040      1050      1060      1070      1080

 1310       1320              1330      1340      1350      1360         X
    TCCTTCAACAGGGAGTTG--------TTGGTGTAGGAGAAGATGTTGAATGGGATGGTCATCGTGAATTC
      ||    |||| |||||        |    | | ||  ||    | | |   |    ||   |||||
    ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
          1090      1100      1110      1120      1130      1140      1150

    AGGACAACAATGGTAACG
        1160      1170

3. US-09-910-186A-9’ (1-1371)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     40  Optimized Score  =    404  Significance = -0.54
Residue Identity =    40%  Matches          =    485  Mismatches   =   626
Gaps             =     91  Conservative Substitutions              =     0

   190       200       210       220       230       240       250       260
    TGAAGATCTGGGAAGCGTAGTAGTAAGTGTTGTTCATTGGCTGGATCTGGAAGATGATGTTGTCGTTGATGT
                            |    | | || |  ||||  |        |||     ||    |  |
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

           270       280       290        300        310       320       330
    CCTTGGTCTGCTCACGCAGACCGATGGCGTAG-ATGTCCTCGGTGGAGTG-GTTGTCGGCGTACATGGTCTC
    | |   |     ||  | || |    ||   | ||    ||    ||  |   ||||    |||     |
    CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
          60        70        80        90       100       110       120

           340       350       360       370       380       390       400
    GTTCTTCATGAACAGGTTGTAGGCCTTGTTGTTGATAGTCATGTCGAAGTACAGGATGTCACCACCTCTGAC
      ||  |||               |||      ||| | || |    ||  |  | |||         | |
    AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGT---------TCAA
       130       140       150       160       170       180

         410       420       430       440       450       460       470
    TCTGGTGTCGTTGGTGTTACCTCTGATACGCTTGATGATGATCTTGTAACCCTCGTTGAAGTCGTTGTTGTT
    |||||  || |      |     | || |    ||     ||| | ||   |||  || |       || |
    TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
    190       200       210       220       230       240       250

       480       490       500       510       520       530       540
    ACGTCTGGTGTTGAAGACGATCTGTCTGGAGTTGGCGTACATGTATCTGTTCAAGTAGTCGATGTTGACCAT
            | | ||     |||       | ||    | ||| | ||||  |||  | |  |   | | ||
    CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAA
  260       270       280       290       300       310       320       330

             550       560       570       580        590       600
    GT--------AGTACTCCTTGTTGTATCTCAGGTCGTTACCCCAGT-AGTCCTTGACGACGTTGGTGTAC-T
     |        |  | | || |||| |    |  ||   ||  | || |   | |   |||  ||  | ||
    CTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACAC
          340       350       360       370       380       390       400

   610       620       630       640       650       660       670       680
    GCAAGGAGTTGAACAGGATGTTGATGTCCTTACCGTCCAACTCCTTGGCGAAGATGTAGAAGTCACGGATCC
     || | | |  |||||  |||||            | ||| | ||    || |||  | |  ||      |
    TCAGGAAATCAAACAGCGTGTTG----------TATTCAAATACTCTCAGATGATCAACATCTCTGACTACA

        410       420                 430       440       450       460

           690       700       710       720       730       740       750
    ACATGTTGATGTTGTCGGAGTCGGAGGTGATCAGACCGGTGTCTGGGATCTTGTTGATCTCGAAGGTGATGG
     ||       | | |  |   |       | ||  |   ||  |            | ||| ||  |
    TCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAAT------------AACTCCAAAATCTACA
      470       480       490       500                   510       520

         760       770       780       790       800       810       820
    TCTTGGAGAAGTTGATACCGGTCAACTCCTTGACCTTGATGGTGTCGATCAGCTTACCGTTGATGTAGATCT
    ||   |      ||||       ||  |  |  ||    |||     |||  |    |        | | |
    TCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTC------TAATAACA
      530       540       550       560       570       580             590

       830       840       850       860       870       880       890
    TCATGTT-ACCCATCATGTTGTTGGTGACGGTGACGAAGAACCACTTGTTGTAACCAGGAGCGTTGTTGGAG
    ||||||| |  |   | | |  | |||||  | ||     ||  || | |  ||          |||| ||
    TCATGTTCAAACTGGACGGTTGTCGTGACACTCAC-CGCTACATCTGGATCAAATACTTCAATCTGTTCGA-
          600       610       620        630       640       650       660

      900       910       920       930       940       950       960
    ATGTCGTAGGAGAAGTTGATGGACTGCTCGGAGTCCTCGTTCTGCTTCAGGGTGAAGACCAGGAAGTTGGAG
        |  || |      ||   |    ||  || ||| || |  |  |  |   ||  |  | |   || |
    ----CAAAGAACTGAACGAAAAAGAAATCAAAGACCT-GTACGACAACCAGTCCAATTCTGGTATCCTGAAA
              670       680       690        700       710       720

    970       980       990      1000      1010      1020      1030
    ATGATACCGATGGACCAACCGGAGTTGTTCTTGACGGAGTCGATGATGGTGTAACCTGGCAAGTTGGAGACC
        |   |   ||| | | | |||    |    || | |  ||| ||    || || | | | |    ||
    GACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTG----AATCT-GTACGATCCGAACA
   730       740       750       760       770           780        790

 1040      1050      1060      1070      1080      1090      1100      1110
    CACTTGTTGATTCTGATCCAGAAGGAGATGGAGAAGGACTCGTACATGGAGTTGTAGACGATGTTCTCGTTC
     |   |||||   | | | |    |  ||        ||  |||| | ||   ||   ||  ||||| |||
    AATACGTTGA-CGTCAACAATGTAGGTATCCGCGGTTACATGTACCT-GAAAGGTCCGCGTGGTTCT-GTTA
      800        810       820       830       840        850       860

            1120      1130      1140      1150      1160      1170      1180
    TGGGT---GACGATGACCTTACCTCTGTCCTCACCGGAGGAACCCAGCTTGAAGTCGAATGGGAAGATTGGG
    ||  |    ||    |||| | ||||  |||   | | || ||| |  |     || |     | |  |  |
    TGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTG
       870       880       890       900       910       920       930

          1190      1200      1210      1220      1230            1240
    TTCAGCTGGACGTCACCCTCCTCGGAGACCTCGGCGTTGTAACCGGAGGTGTCG------ACCAAGGTGTTC
     | |   ||||   | | | | |    |     | ||    | |   | ||| |      || |||     |
    GTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACC
     940       950       960       970       980       990      1000

    1250      1260         1270            1280      1290      1300
    TTACGGTTCTGCAGG---GACAGGATCTTGGAG------TCGTTGATGTTGTTGAAGTACTCGTTGATGATG
     |  || |    | |     |||| |  || ||      || |   || | | ||| | |  |  || |
    GTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTA
  1010      1020      1030      1040      1050      1060      1070      1080

 1310       1320              1330      1340      1350      1360         X
    TCCTTCAACAGGGAGTTG--------TTGGTGTAGGAGAAGATGTTGAATGGGATGGTCATCGTGAATTC
      ||    |||| |||||        |    | | ||  ||    | | |   |    ||   |||||
    ATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGC
          1090      1100      1110      1120      1130      1140      1150

    AGGACAACAATGGTAACG
        1160      1170
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-10.res made by bobryen on Thu 7 Nov 102 14:33:22-PST.


Query sequence being compared:US-09-910-186A-10 (1-450)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

      Results of the initial comparison of US-09-910-186A-10 (1-450) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -                                          *       *        *
S    0-----------------------------------------------------------------
      |   | |     ||      ||     |   |     ||      ||     |  |   |
SCORE 0   | 14    27     41|     55  | 68    82     96|    109 | 123
STDEV    -5      -4      -3         -2      -1        0        1

                              PARAMETERS

Similarity matrix       PAM-150     K-tuple                        1
Threshold level of sim.     16%
Mismatch penalty              1     Joining penalty               20
Gap penalty                5.00     Window size                  450
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                              SEARCH STATISTICS

Scores:                   Mean       Median      Standard Deviation
                           104          89         17.56

Times:                    CPU                    Total Elapsed
                      00:00:00.00                00:00:01.00

Number of residues:                    1704
Number of sequences searched:             3
Number of scores above cutoff:            3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
   1. US-08-123-975A-2 Sequence 2, Application U    850   123   251   1.08    0
                    ****  0 standard deviation from mean ****
   2. US-08-123-975A-5 Sequence 5, Application U    439   103   238  -0.06    0
   3. US-08-123-975A-3 Sequence 3, Application U    415    88   229  -0.91    0


1. US-09-910-186A-10 (1-450)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    123  Optimized Score    =     251  Significance =  1.08
Residue Identity =    25%  Matches            =     121  Mismatches   =   286
Gaps             =     28  Conservative Substitutions                 =    31

                        X       10        20        30        40        50
                        MTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEV
                           ||    |||   | :  | |   |    || |  : | |:| ||| | |
    KLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKV
         380       390  X    400       410       420       430       440

          60        70        80        90       100       110
    SEEGDVQLNPIFPFDFKLGSSGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN------LPGYTII
         | ||    |     :      |: |||| ||::|| :  ||:|||||| |             ||||
    EVYDGVELNDKNQFKLTSSAN----SKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTII
       450       460           470       480       490       500       510

   120       130       140       150       160       170       180       190
    DSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDISNNAPGYNKWFFVTVTNNMMGNMKIYINGKLIDT
       |||||| | |  |  : ||        |: | | |      |    |     | : | ||||||||
    NCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESN
         520       530       540       550       560       570       580

           200       210       220       230       240       250       260
    IKVKELTGINFSKTITFEINKIPDTGLITSDSDNINMWIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWG
      :|:   :     | |      |             | : | ||  ||    |   :    |    ||:||
    TDIKDIREVIANGEIIFKLDGDIDRTQF--------IWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWG
       590       600       610               620       630       640

         270       280       290       300       310       320       330
    NDLRYNKEYYMVNIDYLNRYMYANSRQIVFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVRGGDILYFDMTIN
    | | ||||||| |    | |        |               |  :           |          |
    NPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIV
   650       660       670       680       690       700       710       720

       340               350       360       370       380       390
    NKAYNLFMKNETM--------YADNHSTEDIYAIGLREQTKDINDNIIFQIQPMNNTYYYASQIFKSNFNGE
     |    ::    :        |      |:    :      :    |         ||       |     :
    RKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTD
           730       740       750       760       770       780       790

   400       410       420         430       440       450
    NISGICSIGTYRFRLGGDWYRHNYLVPT--VKQGNYASLLESTSTHWGFVPVSE
     |  |     |      : |:  : :     |              | |:|  |
    EIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
         800       810       820       830       840     X 850


2. US-09-910-186A-10 (1-450)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    103  Optimized Score    =     238  Significance = -0.06
Residue Identity =    25%  Matches            =     115  Mismatches   =   274
Gaps             =     28  Conservative Substitutions                 =    30

            10        20        30        40        50        60        70
    MTIPFNIFSYTNNSLLKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIFPFDFKLGS
                        | |   |    || |  : | |:| ||| | |     | ||    |     :
                       FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSA
                       X       10        20        30        40        50
          80        90       100       110             120       130
    SGEDRGKVIVTQNENIVYNSMYESFSISFWIRINKWVSN------LPGYTIIDSVKNNSGWSIGIISNFLVF
          |: |||| ||::|| :  ||:|||||| |             ||||   |||||| | |  |  :
    N----SKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIW
             60        70        80        90       100       110       120

   140       150       160       170       180       190       200       210
    TLKQNEDSEQSINFSYDISNNAPGYNKWFFVTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEIN
    ||        |: | | |      |    |     | : | ||||||||     :|:   :     | |
    TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLD
          130       140       150       160       170       180       190

           220       230       240       250       260       270       280
    KIPDTGLITSDSDNINMWIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRY
       |             | : | ||  ||    |   :    |    ||:||| | ||||||| |    | |
    GDIDRTQF--------IWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSY
        200               210       220       230       240       250

         290       300       310       320       330       340
    MYANSRQIVFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVRGGDILYFDMTINNKAYNLFMKNETM-------
            |               |  :           |          |  |    ::    :
    IKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVY
    260       270       280       290       300       310       320

     350       360       370       380       390       400       410
    -YADNHSTEDIYAIGLREQTKDINDNIIFQIQPMNNTYYYASQIFKSNFNGENISGICSIGTYRFRLGGDWY
     |      |:    :      :    |         ||       |     : |  |     |      : |
    TYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEY
  330       340       350       360       370       380       390       400

   420         430       440       450
    RHNYLVPT--VKQGNYASLLESTSTHWGFVPVSE
    :  : :     |              | |:|  |
    KDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
          410       420       430    X


3. US-09-910-186A-10 (1-450)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     88  Optimized Score  =     229  Significance = -0.91
Residue Identity  =    27%  Matches          =     117  Mismatches   =   251
Gaps              =     32  Conservative Substitutions               =    30

       20        30     X  40        50        60        70        80
    LKDIINEYFNNINDSKILSLQNRKNTLVDTSGYNAEVSEEGDVQLNPIFPFDFKLGSSGEDRGKVIVTQNEN
                            | |:| | | : :     |   ||      |     :  |: |
                        RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQL--FNLESSKIEVILKNA
                        X       10        20        30          40        50

     90       100       110          120       130       140       150
    IVYNSMYESFSISFWIRINKWVSNLP---GYTIIDSVKNNSGWSIGIISNFLVFTLKQNEDSEQSINFSYDI
    |||||||| || |||||| |          ||||    ||||| :       : ||    :  | : | |
    IVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
            60        70        80        90       100       110       120

     160        170       180       190       200       210       220
    SNNAPGY-NKWFFVTVTNNMMGNMKIYINGKLIDTIKVKELTGINFSKTITFEINKIPDTGLITSDSDNINM
      |   | |:| |||:||| : | ||||||:|||   :  |  |  |  | |      ||
    MINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDT--------HRYI
         130       140       150       160       170       180

    230       240       250       260       270       280       290
    WIRDFYIFAKELDGKDINILFNSLQYTNVVKDYWGNDLRYNKEYYMVNIDYLNRYMYANSRQI---------
    ||: |  | |||  |:|  |:       : ||:||  | | | ||| |    |:|   |   |
    WIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGP
     190       200       210       220       230       240       250

               300       310       320       330       340       350
    ----VFNTRRNNNDFNEGYKIIIKRIRGNTNDTRVRGGDILYFDMTINNKAYNLFMKNETMYADNHSTEDIY
               |     | | |||:      |  ||  |  |    : || | |        |     | |
    RGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRL-----ATNASQAGVEKIL
```

```
260       270       280       290       300       310            320

360       370       380       390       400       410       420       430
 AIGLREQTKDINDNIIFQIQPMNNTYYYASQIFKSNFNGENISGICSIGTYRFRLGGDWYRHNYLVPTVKQG
 :             ::                   |   :             :| :            :
 SALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTL
   330       340       350       360       370       380       390

        440       450
 NYASLLESTSTHWGFVPVSE
   :         ||  |
 GCSWEFIPVDDGWGERPL
 400       410    X
```

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O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-11.res made by bobryen on Thu 7 Nov 102 14:43:36-PST.


Query sequence being compared:US-09-910-186A-11 (1-1374)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-11 (1-1374) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                                                      *
S    0----------------------------------------------------------------------
      |      |  |    |     | |   |  |  |   ||     |    | |   |  | |    |
SCORE 0     50 |  101    151   |202   | 252|   303   353    |404 |  454
STDEV         -9   -8    -7    -6    -5   -4    -3   -2    -1    0

                                PARAMETERS

Similarity matrix      Unitary   K-tuple                    4
Mismatch penalty             1   Joining penalty           30
Gap penalty               5.00   Window size              500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                                SEARCH STATISTICS

Scores:                  Mean       Median      Standard Deviation
                          431         387           39.26

Times:                  CPU                    Total Elapsed
                     00:00:00.00               00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                         Init.  Opt.
Sequence Name     Description                    Length Score  Score  Sig. Frame
----------------------------------------------------------------------------------
  1. US-08-123-975A-4 Sequence 4, Application U   1338   454    624   0.59   0
  2. US-08-123-975A-1 Sequence 1, Application U   1338   454    624   0.59   0
                **** 1 standard deviation below mean ****
  3. US-08-123-975A-6 Sequence 6, Application U   1351   386    621  -1.15   0

1. US-09-910-186A-11 (1-1374)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =   454  Optimized Score  =   624  Significance =  0.59
Residue Identity =   50%  Matches          =   669  Mismatches   =   619
Gaps             =    49  Conservative Substitutions          =     0

     60        70    X   80        90        100       110       120
 CCATTCAACATCTTCTCCTACACCAACAACTCCTTGT-TGAAGGACATCATCAACGAGTACTTCAACTCCAT
                     | | | | |   || || ||  |   | | |||  || ||| ||||   |||
                     CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                     X       10        20        30        40        50

   130       140       150       160       170       180       190
 CAACGACTCCAAGATCTTGTCCTTGCAGAACAAGAAGAACGCCTTGGTCGACACCTCCGGTTACAACGCCGA
 || | |  ||   ||| ||  | |||   || |    ||   | || |||||   ||  | |||    || |
 CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
       60        70        80        90       100       110       120

 200       210       220       230       240       250       260
 GGTCAGAGTCGGTGACAACGTCCAGTTGAACACCATCTACACCAACGACTTCAAGTTGTCCTCTTCCG---G
   |||   |||||   || ||  | ||  |  | ||| |||  ||  |  || || ||| |  |   |
 AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
    130       140       150       160       170       180       190

  270       280       290       300       310       320       330
 TGACAAGATCATCGTCAACTTGAACAACAACATCTTGTACTCCGCCATCTACGAGAACTCCTCTGTCTCCTT
 |  ||| |||   || | | |||| ||    ||| | |||  | | || ||||| |||| |||   ||||||
 TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTT
  200       210       220       230       240       250       260

340       350       360          370          380       390       400
 CTGGATCAAGATCTCCAAGGACTTGA---CCAACTCCC---ACAACGAGTACACCATCATCAACTCCATCGA
 |||||||   ||| | ||  |||| |   ||| ||| |   |||| || |||||||||||||||| ||| ||
 CTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGA
270       280       290       300       310       320       330       340

    410       420       430       440       450       460       470
 GCAGAACTCCGGTTGGAAGTTGTGTATCCGTAACGGTAACATCGAGTGGATCTTGCAGGACGTCAACCGTAA
   | || || ||||||||  | | | |     ||||| | |||   ||||   ||||||||    |    |
 AAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAAT
        350       360       370       380       390       400       410

  480       490       500       510       520       530       540
 GTACAAGTCCTTGATCTTCGACTACTCCGAGTCCTTGTCCCACACCGGTTACACCAACAAGTGGTTCTTCGT
   |  ||    |  | ||| | |||||  ||    |   |  | | |  |||| |||    ||| |||||||
 CAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGT
      420       430       440       450       460       470       480

550       560       570       580       590       600       610       620
 CACCATCACCAACAACATCATGGGTTACATGAAGTTGTACATCAACGGTGAGTTGAAGCAGTCCCAGAAGAT
  ||||||||||||||     ||  | ||   ||  | |||||||||||     |||   |     |   |||
 TACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGAT
    490       500       510       520       530       540       550

        630       640       650       660       670       680       690
 CGAGGACCTGGACGAGGTCAAGCTGGACAAGACCATCGTCTTCGGTATCGACGAGAACATCGACGAGAACCA
 |    | ||||   |  || |       || | |||| | |||    | ||||        |||    |||
 CTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCG
  560       570       580       590       600       610       620

      700       710       720       730       740       750       760
 GATGTTGTGGATTCGTGACTTCAACATCTTCTCCAAGGAGCTGTCCAACGAGGACATCAACATCGTCTACGA
      | |||||     |||||||  | |||  ||| || |||  | |  | || |||||   | | |||||
    CTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGA
 630       640       650       660       670       680       690       700

     770       780       790       800       810       820       830
    GGGTCAGATCCTGAGGAACGTCATCAAGGACTACTGGGGTAACCCACTGAAGTTCGACACCGAGTACTACAT
        |||  |          || | || |||| ||||||| ||   ||| ||| |||||    |||||||||
    CAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACAT
           710       720       730       740       750       760       770

   840       850       860       870       880       890         900
    CATCAACGACAACTACATCGACCGTTACATCGCCCCAGAGTCCAACGTCCTGGTC--CTGGTCCAGTACCCT
      | ||     || |     ||   ||| | | |   |    ||| ||     ||  | | | ||    |||
    GCTGAATCTGTACGATCCGAACAAATACGTTGAC---GTCAACAATGTAGGTATCCGCGGTTACATGTACCT
         780       790       800          810       820       830       840

   910       920       930       940       950       960       970
    GACCTGTCCAAGCTGTACACCGGTAACCCTATCACCATCAAGTCCGTCTCCGACAAGAACCCTTACTCCCGT
    ||   ||||  |  ||   | | ||   ||| || |||| |      |||   |  | ||| |    ||
    GAAAGGTCCGCGTGGT--TCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAA
          850         860       870       880       890       900       910

980                     990      1000      1010      1020      1030
    ATCCTGAAC------------GGTGACAACATCATCCTGCACATGCTGTACAACTCCCGTAAGTACATGATC
     || | | |              ||  ||||    |     | | |   ||||    |||   |||   |||
    TTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATAC---ATC
          920       930       940       950       960       970          980

1040        1050      1060      1070      1080      1090      1100      1110
    ATCCGTGACACCGACACCATCTACGCCACCCAGGGTGGTGAGTGTTCCCAGAACTGTGTCTACGCCCTGAAG
    |    ||      | | ||   |   |   | || |    |   ||| |||    ||||  |     |   |
    AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTG
          990      1000      1010      1020      1030      1040      1050

         1120      1130      1140      1150      1160      1170      1180
    -CTGCAGTCCAACCTGGGTAACTACGGTATCGGTATCTTCTCCATCAAGAACATCGTCTCCAAGAACAAGTA
     ||||  |  ||     | |  |  |  ||| || ||   |   |  |    ||    ||||||||| |  |
    TCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTA----ATGAAATCCAAGAACGACCA
      1060      1070      1080      1090      1100          1110        1120

         1190      1200      1210      1220      1230      1240      1250
    CTGCTCCCAGATCTTCTCCTCCTTCCGTGAGAACACCATGCTGCTGGCCGACATCTACAAGCCTTGGCGTTT
      |   |   | |   | |    |   |  | |   ||          ||| |||          |
    GGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCA
          1130      1140      1150      1160      1170      1180      1190

       1260      1270      1280      1290                1300      1310
    CTCCTTCAAGAACGCCTACACTCCTGTCGCCGTCACCAACTAC--------GAGACCAAGCTGCTGTCCACC
    |   ||||| ||   |   |  |  || ||   || |   |||        ||    | | | || ||   |
    CCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCAC
        1200      1210      1220      1230      1240      1250      1260

       1320      1330      1340      1350      1360      1370   X
    TC----CTCCTTCTGGAAGTTCATCTCCCGTGACCCAGGTTGGGTCGAGTAATAGGAATTC
    ||     | ||  ||| |||||||| |   |||    |||||||  ||      |   |
    TCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGC
      1270      1280      1290      1300      1310      1320    X 1330

    TT


2. US-09-910-186A-11 (1-1374)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    454  Optimized Score  =    624  Significance =  0.59
Residue Identity  =    50%  Matches          =    669  Mismatches   =   619
Gaps              =     49  Conservative Substitutions             =     0

        60        70    X   80        90        100       110       120
    CCATTCAACATCTTCTCCTACACCAACAACTCCTTGT-TGAAGGACATCATCAACGAGTACTTCAACTCCAT
                        | | | | |   || || ||  |   | | |||  || ||| ||||   |||
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X        10        20        30        40        50
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    130       140       150       160       170       180       190
    CAACGACTCCAAGATCTTGTCCTTGCAGAACAAGAAGAACGCCTTGGTCGACACCTCCGGTTACAACGCCGA
    || | |  ||   ||| ||  | |||   || |    ||   | || |||||   ||  | |||    || |
    CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
         60        70        80        90       100       110       120

  200       210       220       230       240       250       260
    GGTCAGAGTCGGTGACAACGTCCAGTTGAACACCATCTACACCAACGACTTCAAGTTGTCCTCTTCCG---G
      |||   |||||   || ||  | ||  |  | ||| |||  ||  |  || || ||| |  |   |
    AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
      130       140       150       160       170       180       190

   270       280       290       300       310       320       330
    TGACAAGATCATCGTCAACTTGAACAACAACATCTTGTACTCCGCCATCTACGAGAACTCCTCTGTCTCCTT
    |  ||| |||   || | | |||| ||    ||| | |||  | | || ||||| |||| |||   ||||||
    TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTT
   200       210       220       230       240       250       260

340       350       360           370          380       390       400
    CTGGATCAAGATCTCCAAGGACTTGA---CCAACTCCC---ACAACGAGTACACCATCATCAACTCCATCGA
    |||||||   ||| | ||  |||| |   ||| ||| |   |||| || |||||||||||||||| ||| ||
    CTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGA
270       280       290       300       310       320       330       340

    410       420       430       440       450       460       470
    GCAGAACTCCGGTTGGAAGTTGTGTATCCGTAACGGTAACATCGAGTGGATCTTGCAGGACGTCAACCGTAA
      | || || ||||||||  | | | |     ||||| | |||   ||||   ||||||||    |    |
    AAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAAT
           350       360       370       380       390       400       410

   480       490       500       510       520       530       540
    GTACAAGTCCTTGATCTTCGACTACTCCGAGTCCTTGTCCCACACCGGTTACACCAACAAGTGGTTCTTCGT
      |  ||    |  | ||| | |||||  ||    |   |  | | |  |||| |||    ||| |||||||
    CAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGT
        420       430       440       450       460       470       480

550       560       570       580       590       600       610       620
    CACCATCACCAACAACATCATGGGTTACATGAAGTTGTACATCAACGGTGAGTTGAAGCAGTCCCAGAAGAT
     ||||||||||||||     ||  | ||   ||  | |||||||||||     |||   |     |   |||
    TACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGAT
      490       500       510       520       530       540       550

          630       640       650       660       670       680       690
    CGAGGACCTGGACGAGGTCAAGCTGGACAAGACCATCGTCTTCGGTATCGACGAGAACATCGACGAGAACCA
    |    | ||||   |  || |       || | |||| | |||    | ||||        |||    |||
    CTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCG
    560       570       580       590       600       610       620

        700       710       720       730       740       750       760
    GATGTTGTGGATTCGTGACTTCAACATCTTCTCCAAGGAGCTGTCCAACGAGGACATCAACATCGTCTACGA
         | |||||     |||||||  | |||  ||| || |||  | |  | || |||||   | | |||||
    CTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGA
 630       640       650       660       670       680       690       700

     770       780       790       800       810       820       830
    GGGTCAGATCCTGAGGAACGTCATCAAGGACTACTGGGGTAACCCACTGAAGTTCGACACCGAGTACTACAT
        |||  |          || | || |||| ||||||| ||   ||| ||| |||||    |||||||||
    CAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACAT
           710       720       730       740       750       760       770

   840       850       860       870       880       890         900
    CATCAACGACAACTACATCGACCGTTACATCGCCCCAGAGTCCAACGTCCTGGTC--CTGGTCCAGTACCCT
      | ||     || |     ||   ||| | | |   |    ||| ||     ||  | | | ||    |||
    GCTGAATCTGTACGATCCGAACAAATACGTTGAC---GTCAACAATGTAGGTATCCGCGGTTACATGTACCT
         780       790       800          810       820       830       840

   910       920       930       940       950       960       970
    GACCTGTCCAAGCTGTACACCGGTAACCCTATCACCATCAAGTCCGTCTCCGACAAGAACCCTTACTCCCGT
    ||   ||||  |  ||   | | ||   ||| || |||| |      |||   |  | ||| |    ||
    GAAAGGTCCGCGTGGT--TCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAA
          850         860       870       880       890       900       910
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980                   990      1000      1010      1020      1030
 ATCCTGAAC------------GGTGACAACATCATCCTGCACATGCTGTACAACTCCCGTAAGTACATGATC
  || | | |              ||  ||||     |     | | |   ||||    |||   |||   |||
 TTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATAC---ATC
       920       930       940       950       960       970          980

1040     1050      1060      1070      1080      1090      1100      1110
 ATCCGTGACACCGACACCATCTACGCCACCCAGGGTGGTGAGTGTTCCCAGAACTGTGTCTACGCCCTGAAG
 |    ||      | | ||   |   |   | || |    |   ||| |||    ||||  |     |   |
 AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTG
        990      1000      1010      1020      1030      1040      1050

        1120      1130      1140      1150      1160      1170      1180
 -CTGCAGTCCAACCTGGGTAACTACGGTATCGGTATCTTCTCCATCAAGAACATCGTCTCCAAGAACAAGTA
  ||||  |  ||     | |  |  |  ||| || ||   |   |  |    ||    ||||||||| |  |
 TCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTA----ATGAAATCCAAGAACGACCA
     1060      1070      1080      1090      1100          1110      1120

       1190      1200      1210      1220      1230      1240      1250
 CTGCTCCCAGATCTTCTCCTCCTTCCGTGAGAACACCATGCTGCTGGCCGACATCTACAAGCCTTGGCGTTT
   |   |   | |   | |    |   |  | |   ||          ||| |||          |
 GGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCA
       1130      1140      1150      1160      1170      1180      1190

     1260      1270      1280      1290              1300      1310
 CTCCTTCAAGAACGCCTACACTCCTGTCGCCGTCACCAACTAC--------GAGACCAAGCTGCTGTCCACC
 |   ||||| ||   |   |  |  || ||   || |   |||        ||    | |  | || ||   |
 CCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCAC
     1200      1210      1220      1230      1240      1250      1260

     1320      1330      1340      1350      1360      1370  X
 TC----CTCCTTCTGGAAGTTCATCTCCCGTGACCCAGGTTGGGTCGAGTAATAGGAATTC
 ||     | ||  ||| ||||||||| |   |||    |||||||  ||       |   |
 TCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGC
   1270      1280      1290      1300      1310      1320    X 1330

 TT


3. US-09-910-186A-11 (1-1374)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    386  Optimized Score   =    621  Significance = -1.15
Residue Identity =    51%  Matches           =    699  Mismatches   =   557
Gaps             =    104  Conservative Substitutions              =     0

      80        90   X   100       110       120       130       140
 ACACCAACAACTCCTTGTTGAAGGACATCATCAACGAGTACTTCAACTCCATCAACGACTCCAAGATCTTGT
                     | ||   ||| |||  |  | | | |   | | ||| |    |  ||| ||
                     ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAA---TATCATCCTGA
                     X       10        20        30           40

   150       160       170       180       190       200       210
 CCTTGCAGAACAAGAAGAACGCCTTGGTCGACACCTCCGGTTACAACGCCGAGGTCAGAGTCGGTGACAACG
  | |||   ||||  | |||    || ||||    || ||||||   ||  | ||   |||    |||    |
 ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTG
50        60        70        80        90       100       110       120

 220       230       240       250       260       270          280
 TCCAGTTGAACACCATCTACACCAACGACTTCAAGTTGTCCTCTTCCGGTGAC---AAGATCATCGTCAACT
 |  |  ||||        ||   ||| | ||||  || |||||||| | ||   ||||||   || |
 TTGAACTGAA------TGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTC
       130             140       150       160       170       180

  290       300       310       320       330       340       350
 TGAACAACAACATCTTGTACTCCGCCATCTACGAGAACTCCTCTGTCTCCTTCTGGATCAAGATCTCCAAGG
  |||  | ||||||| | | |  | || | | |  | ||| |||||| |||||||||||||   ||| | ||
 AGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAAT
 190       200       210       220       230       240       250

360                      370       380       390       400       410
 ACTTGACC---------------AACTCCCACAACGAGTACACCATCATCAACTCCATCGAGCAGAACTCCG
 ||  || |                ||  ||||||| || ||||||||||||||||| |||  || | ||||| |
 ACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTG
260      270       280       290       300       310       320       330

   420       430          440       450       460       470       480
 GTTGGAAGTTGTGTATCC---GTAACGGTAACATCGAGTGGATCTTGCAGGACGTCAACCGTAAGTACAAGT
 |||||||| | |  ||||    ||||| ||| ||||   ||||   ||   ||   ||  ||||| |||||  ||| |
 GTTGGAAGATCTCCATCCGCGGTAACCGTATCATC---TGGACTCTGATCGATATCAACGGTAAGACCAAAT
       340       350       360          370       380       390       400

    490       500       510       520       530       540       550
 CCTTGATCTTCGACTACTCCGAGTCCTTGTCCCACACCGGTTACACCAACAAGTGGTTCTTCGTCACCATCA
 |  |  |||||||| ||  |            |  | | |  |||| |||    |||||||||||| |||||||
 CTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCA
        410       420       430       440       450       460       470

  560       570       580       590       600       610       620
 CCAACAACATCATGGGTTACATGAAGTTGTACATCAACGGTGAGTTGAAGCAGTCCCAGAAGATCGAGGACC
 |||| ||   | ||    |    ||  | |||||||||||| |  || |           | ||| | |||
 CCAATAA---CCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACA
      480          490       500       510       520       530       540

630       640       650       660       670       680       690       700
 TGGACGAGGTCAAGCTGGACAAGACCATCGTCTTCGGTATCGACGAGAACATCGACGAGAACCAGATGTTGT
 |    || || |      ||      ||| |||||    | ||||   |||||||    | |||| |  | |
 TCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCT
       550       560       570       580       590       600       610

        710       720       730       740       750       760       770
 GGATTCGTGACTTCAACATCTTCTCCAAGGAGCTGTCCAACGAGGACATCAACATCGTCTACGAGGGTCAGA
 ||||     |||||  |||||||  ||  || |||||  |     | ||| |       ||| ||   |||
 GGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGT
     620       630       640       650       660       670       680

      780       790       800       810       820       830       840
 TCCTGAGGAACGTCATCAAGGACTACTGGGGTAACCCACTGAAGTTCGACACCGAGTACTACATCATCAACG
          |   | | || |||| ||||||||| || || | || | ||  || ||||| ||  ||||  |
 CTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATG
   690       700       710       720       730       740       750

    850       860       870       880       890       900       910
 ACAACTACATCGACCGTTACATCGCCCCAGAGTCCAACGTCCTGGTCCTGGTCCAGTACCCTGACCTGTCCA
       |||   ||  |||||||   |   ||    |  | |||  ||||  |  | ||||||  || |
 CTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGT--TGGTGAA--ATCCTGACTCGTTCC
 760       770       780       790       800         810         820

  920       930       940       950       960       970       980
 AGCTGTACACCGGTAACCCTATCACCATCAAGTCCGTCTCCGACAAGAACCCTTACTCCCGTATCCTGAACG
 |    |||| |   ||| |||    |||||| | | |  ||    | | | |  | |         ||| |
 A--AATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTC
     830       840       850       860       870       880       890

990      1000      1010      1020      1030      1040       1050
 GTGACAACATCATCCTGCACATGCTGTACAACTCCCGTAAGTACATGATCATCCGT-GACACCGACACCATC
 |  |    | |   | |  |||     |  ||   |||| ||| |  |   | | |  ||   |||  | ||
 GCAAATCTAACTCTCAGTCCATCAATGATGAC-ATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTC
   900       910       920        930       940       950       960

1060    1070       1080      1090      1100      1110      1120      1130
 TACGCCACCCAGG-GTGGTGAGTGTTCCCAGAACTGTGTCTACGCCCTGAAGCTGCAGTCCAACCTGGGTAA
  ||   |  ||||  ||| || | | | |   ||   |       ||||  | |   |    |   |
 AACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGC--TTTTCCTGG
  970       980       990      1000      1010      1020        1030

       1140       1150      1160      1170      1180      1190      1200
 CTACGGTATC-GGTATCTTCTCCATCAAGAACATCGTCTCCAAGAACAAGTACTGCTCCCAGATCTTCTCCT
 || || | ||  | |  |  |    || | |||| | ||   |  ||  | |||  |   ||     || ||
 CTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACT
 1040      1050      1060      1070      1080      1090      1100

                   1210      1220                     1230
 CCTTCC-------------GTGAGAACACCATGCTGCTGGC--------------CGACATCTAC-------
 | | ||             |  |||  |  |  || ||| |              ||  ||| ||
    CTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCT
  1110      1120      1130      1140      1150      1160      1170      1180

 1240      1250      1260      1270      1280      1290      1300
    AAGCCTTGGCGTTTCTCCTTCAAGAACGCCTACACTCCTGTCGCCGTCACCAACTACGAGACCAAG------
    | |  |  |   |  |  |  |||||  |  | ||| || ||  | || |||| |   |    |||
    ACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACT-TCTGCATCTCCAAATGGTACCTGAAGGAAGTT
          1190      1200      1210       1220      1230      1240      1250

           1310               1320      1330      1340      1350      1360
    ------CTGCTGTCCACC---------TCCTCCTTCTGGAAGTTCATCTCCCGTGACCCAGGTTGGGTCGAG
             | || || |            | |   ||| |||||||| |    |||  |||||||  |||
    AAACGCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAA
         1260      1270      1280      1290      1300      1310      1320

        1370   X
    TAATAGGAATTC
    || ||     |
    TAGTAACCTCTAGAGTCGAGGCCTGCAG
       1330    X 1340      1350
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-11-inv.res made by bobryen on Thu 7 Nov 102 14:44:07-PST.


Query sequence being compared:US-09-910-186A-11' (1-1374)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-11' (1-1374) with:
        File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                              *
N     -
C     -
E     -                                                 *
S    0--------------------------------------------------------------------
      |     ||      |      | |    | |    |  |   |   |  |     ||     ||
SCORE 0     |5      10     15 |   20 |    26  |    31  | 36     41     46
STDEV       -6      -5        -4     -3      -2       -1         0      1


                                PARAMETERS

Similarity matrix      Unitary    K-tuple                  4
Mismatch penalty             1    Joining penalty         30
Gap penalty               5.00    Window size            500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                  Mean        Median      Standard Deviation
                           42            37             5.77

Times:                    CPU                    Total Elapsed
                    00:00:00.00                   00:00:00.00

Number of residues:                   4027
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                         Init. Opt.
Sequence Name      Description                     Length Score Score  Sig. Frame
---------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338     46   308    0.69    0
   2. US-08-123-975A-1 Sequence 1, Application U   1338     46   308    0.69    0
                  **** 1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351     36   296   -1.04    0

1. US-09-910-186A-11' (1-1374)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     46  Optimized Score =     308  Significance =  0.69
Residue Identity =    41%  Matches         =     366  Mismatches   =   437
Gaps             =     71  Conservative Substitutions          =     0

           520       530       540       550       560       570       580
    GTAACGGTCGATGTAGTTGTCGTTGATGATGTAGTACTCGGTGTCGAACTTCAGTGGGTTACCCCAGTAGTC
                        |       |||        | |||| | ||||| ||  |    | || |
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

         590       600       610       620       630       640       650
    CTTGATGACGTTCCTCAGGATCTGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAA
    | | |  || | | ||     |||| |||     ||||     ||  |||  | |   | ||   | |  |
    CATCAATACCTCCATC-----CTGAACCTGCGCTACGAATCCAATCACCTGATCG---ACCTGTCTCGCTAC
          60             70        80        90       100          110

       660       670       680       690       700       710       720
    GATGTTGAAGTCACGAATCCACAACATCTGGTTCTCGTCGATGTTCTCGTCGATACCGAAGACGATGGTCTT
    | |       ||   |||| ||| |    ||||||     | |||  | ||||| |    ||| |   ||
    GCT-------TCCAAAATCAACATC----GGTTCT----AAAGTTAACTTCGATCCGATCGACAAGAATCAG
                120       130           140           150       160       170

     730       740       750       760       770       780       790
    GTCCAGCTTGACCTCGTCCAGGTCCTCGATCTTCTGGGACTGCTTCAACTCACCGTTGATGTACAACTTCAT
     |||||||   |    |  |  || || |   ||   |    | | ||     |  |  | |||||||  ||
    ATCCAGCTGTTCAATCTGGA-ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTAT
        180       190        200       210       220       230       240

   800                810       820       830             840       850
    GTA---------ACCCATGATGTTGTTGGTGATGGTGACGAA------GAACCACTTGTTGGTGTAACCGGT
    |||           |||     || | | |     |  ||||       |||  | | |   || |    |
    GTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGA
       250       260       270       280       290       300       310

      860       870       880       890       900       910       920
    GTGGGACAAGGACTCGGAGTAGTCGAAGATCAAGGACTTGTACTTACGGTTGACGTCCTGCAAGATCCACTC
     |    ||    |        |   || |     |  | | |  ||    |||  | | |  | |||  ||
    ATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTG
     320       330       340       350       360       370       380

    930       940       950       960       970       980       990
    GATGTTACCGTTACGGATACACAACTTCCAACCGGAGTTCTGCTCGATGGAGTTGATGATGGTGTACTCGTT
    ||   | | |      |  ||  |  || ||| |    |    |  |   | |    |||| |  ||    |
    GACTCTGCAG---GACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAAC---AT
   390          400       410       420       430       440       450

 1000      1010      1020      1030      1040      1050      1060      1070
    GTGGGAGTTGGTCAAGTCCTTGGAGATCTTGATCCAGAAGGAGACAGAGGAGTTCTCGTAGATGGCGGAGTA
     |  || |   ||||   || |    || | | |   |   | |       |      |  |      |
    CTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACAT
       460       470       480       490       500       510       520

         1080      1090      1100      1110      1120      1130      1140
    CAAGATGTTGTTGTTCAAGTTGACGATGATCTTGTCACCGGAAGAGGACAACTTGAAGTCGTTGGTGTAGAT
    |||        || || |   ||    |||||      |  |   ||  ||| |  |  | |      | ||
    CAACGGCCGTCTGATCGACCAGAAACCGATCT------CCAATCTGGGTAACATCCACGCTTCTAATAACAT
     530       540       550             560       570       580       590

       1150       1160      1170      1180      1190      1200      1210
    GGTGTTC-AACTGGACGTTGTCACCGACTCTGACCTCGGCGTTGTAACCGGAGGTGTCGACCAAGGCGTTCT
      ||||| ||||||||| |      ||| || ||| |  | |    | |  |    || | |    ||
    CATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCG---A
         600       610       620       630       640       650       660

      1220      1230      1240      1250           1260      1270      1280
    TCTTGTTCTGCAAGGACAAGATCTTGGAGTCGTTGATG-----GAGTTGAAGTACTCGTTGATGATGTCCTT
        |  ||| | | | ||||  |   || | |  | |      |||  | |      |  |||    |||
    CAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTT
          670       680       690       700       710       720       730

         1290      1300               1310      1320      1330      1340
    CAACAAGGAGTTGTTGGTGTAGGAGA---------AGATGTTGAATGGCATGGTGTTCTCGAAGGACTCGTT
    |      || |   ||  ||| || |         | ||| |||||  |     | ||   |   |  ||||
    CTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAAT--CTGTACGATCCGAACAAATACGTT
        740       750       760       770         780       790       800

      1350      1360      1370   X
    GACCTTAGCCTTCAAACGCATCGTGAATTC
    ||| | | |  |  |      || |  | |
    GACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCG
        810       820       830  X    840       850


2. US-09-910-186A-11' (1-1374)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     46  Optimized Score  =    308  Significance =  0.69
Residue Identity =    41%  Matches          =    366  Mismatches   =   437
Gaps             =     71  Conservative Substitutions             =     0

           520       530       540       550       560       570       580
    GTAACGGTCGATGTAGTTGTCGTTGATGATGTAGTACTCGGTGTCGAACTTCAGTGGGTTACCCCAGTAGTC
                        |       |||        | |||| | ||||| ||  |    | || |
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

         590       600       610       620       630       640       650
    CTTGATGACGTTCCTCAGGATCTGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAA
    | | |  || | | ||      |||| |||     ||||     ||  |||  | |   | ||   | |  |
    CATCAATACCTCCATC-----CTGAACCTGCGCTACGAATCCAATCACCTGATCG---ACCTGTCTCGCTAC
          60             70        80        90       100          110

       660       670       680       690       700       710       720
    GATGTTGAAGTCACGAATCCACAACATCTGGTTCTCGTCGATGTTCTCGTCGATACCGAAGACGATGGTCTT
    | |       ||   |||| ||| |    ||||||     | |||  | ||||| |    ||| |   ||
    GCT-------TCCAAAATCAACATC----GGTTCT----AAAGTTAACTTCGATCCGATCGACAAGAATCAG
            120       130           140           150       160       170

     730       740       750       760       770       780       790
    GTCCAGCTTGACCTCGTCCAGGTCCTCGATCTTCTGGGACTGCTTCAACTCACCGTTGATGTACAACTTCAT
     |||||||   |    |  |  || || |   ||   |    | | ||     |  |  |  |||||||  ||
    ATCCAGCTGTTCAATCTGGA-ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTAT
        180       190        200       210       220       230       240

   800                810       820       830             840       850
    GTA---------ACCCATGATGTTGTTGGTGATGGTGACGAA------GAACCACTTGTTGGTGTAACCGGT
    |||           |||     || | | |     |  ||||       |||  | | |   || |    |
    GTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGA
       250       260       270       280       290       300       310

      860       870       880       890       900       910       920
    GTGGGACAAGGACTCGGAGTAGTCGAAGATCAAGGACTTGTACTTACGGTTGACGTCCTGCAAGATCCACTC
     |    ||     |        |   || |     |  | | |  ||    |||  | | |  | |||  ||
    ATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTG
     320       330       340       350       360       370       380

    930       940       950       960       970       980       990
    GATGTTACCGTTACGGATACACAACTTCCAACCGGAGTTCTGCTCGATGGAGTTGATGATGGTGTACTCGTT
    ||   | | |      |  ||  |  || ||| |    |  |   | |    ||||| |  ||    |
    GACTCTGCAG---GACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAAC---AT
   390          400       410       420       430       440       450

 1000      1010      1020      1030      1040      1050      1060      1070
    GTGGGAGTTGGTCAAGTCCTTGGAGATCTTGATCCAGAAGGAGACAGAGGAGTTCTCGTAGATGGCGGAGTA
     |  || |   ||||   || |    || | | |   |   | |       |      |  |      |
    CTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACAT
       460       470       480       490       500       510       520

         1080      1090      1100      1110      1120      1130      1140
    CAAGATGTTGTTGTTCAAGTTGACGATGATCTTGTCACCGGAAGAGGACAACTTGAAGTCGTTGGTGTAGAT
    |||         || || |   ||    |||||      |  |   ||  ||| |  |  |  |      | ||
    CAACGGCCGTCTGATCGACCAGAAACCGATCT------CCAATCTGGGTAACATCCACGCTTCTAATAACAT
     530       540       550             560       570       580       590

       1150       1160      1170      1180      1190      1200      1210
    GGTGTTC-AACTGGACGTTGTCACCGACTCTGACCTCGGCGTTGTAACCGGAGGTGTCGACCAAGGCGTTCT
      ||||| ||||||||| |      ||| || ||| |  |  |    | |  |    || | |    ||
    CATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCG---A
         600       610       620       630       640       650       660

      1220      1230      1240      1250           1260      1270      1280
    TCTTGTTCTGCAAGGACAAGATCTTGGAGTCGTTGATG-----GAGTTGAAGTACTCGTTGATGATGTCCTT
        |  ||| | | | ||||  |   || | |  | |      |||  | |      |  |||    |||
    CAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTT
          670       680       690       700       710       720       730

         1290      1300               1310      1320      1330      1340
    CAACAAGGAGTTGTTGGTGTAGGAGA---------AGATGTTGAATGGCATGGTGTTCTCGAAGGACTCGTT
    |      || |   ||  ||| || |         | ||| |||||  |     | ||   |   |  ||||
    CTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAAT--CTGTACGATCCGAACAAATACGTT
        740       750       760       770         780       790       800

      1350      1360      1370   X
    GACCTTAGCCTTCAAACGCATCGTGAATTC
    ||| | | |  |  |      || |  | |
    GACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCG
        810       820       830  X    840       850


3. US-09-910-186A-11' (1-1374)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     36  Optimized Score  =    296  Significance = -1.04
Residue Identity =    40%  Matches          =    349  Mismatches   =   468
Gaps             =     44  Conservative Substitutions             =     0

   520       530       540       550       560       570       580       590
    CGATGTAGTTGTCGTTGATGATGTAGTACTCGGTGTCGAACTTCAGTGGGTTACCCCAGTAGTCCTTGATGA
                        |||   | |      |  ||  | |          |   | |        | |||  |
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGA--A
                        X       10        20        30        40          50

           600       610       620       630       640       650       660
    CGTTCCTCAGGATCTGACCCTCGTAGACGATGTTGATGTCCTCGTTGGACAGCTCCTTGGAGAAGATGTTGA
    | | | | |  |    | |    |   |||| |   ||    || ||   |  |    | | || | |
    CCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGT
            60        70        80        90       100       110       120

         670       680       690       700       710       720       730
    AGTCACGAATCCACAACATCTGGTTCTCGTCGATGTTCTCGTCGATACCGAAGACGATGGTCTTGTCCAGCT
     |    ||||  |||| | |  ||||     ||  |  ||  | |   | ||||     || ||   |||
    TGAACTGAAT-GACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGA--TCCGTGTTACTCAGAA
         130        140       150       160       170         180       190

       740       750         760       770       780       790       800
    TGACCTCGTCCAGGTC--CTCGATCTTCTGGGACTGCTTCAACTCACCGTTGATGTACAACTTCATGTA-AC
    | |   | ||    ||  ||  |  | |||  ||||| ||     ||    | |||    | |   |  || |
    TCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAA
          200       210       220       230       240       250       260

        810       820       830       840       850       860       870
    CCATGATGTTGTTGGTGATGGTGACGAAGAACCACTTGTTGGTGTAACCGGTGTGGGACAAGGACTCGGAGT
      | || | | |     ||     | |  |   |          | | | |  | | | ||  |||| |
    GAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCAT-GAAGAATAACTCTG---
        270       280       290       300       310        320       330

      880       890       900       910         920       930       940
      AGTCGAAGATCAAGGACTTGTACTTACGGTTGACG--TCCTGCAAGATCCACTCGATGTTACCGTTACGGAT
        | |||||||       | |    ||||   ||  || |      ||   ||||| | | || || |
      GTTGGAAGATC-------TCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACC
            340              350       360       370       380       390

        950       960       970       980       990      1000      1010
      ACACAACTTCCAACCGGAGTTCTGCTCGATGGAGTTGATGATGGTGTACTCGTTGTGGGAGTTGGTCAAGTC
      | |    |      || |       ||  || ||   ||    |  |||       |   |||  ||    |
      AAATCTGTATTCTTCGAATACAACATCCGTGAAG-ACATCTCTGAATACATCAATCGCTGGTTCTTCGTTAC
       400       410       420       430        440       450       460

     1020      1030      1040      1050      1060      1070      1080
      CTTGGAGATCTTGATCCAGAAGGAGACAGAGGAGTTCTCGTAGATGGCGGAGTACAAGATGTTGTTGTTCAA
      | |    |      |  | || |  | |    |  ||      |    ||| |  |  ||   |   |  ||
      CATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTA--ATACCGACATCAAA
      470       480       490       500       510       520        530

   1090      1100        1110      1120      1130      1140      1150
      GTTGACGATGATCTTGTCAC--CGGAAGAGGACAACTTGAAGTCGTTGGTGTAGATGGTGTTCAACTGGACG
      |    |  |||  || || |    |  ||   || ||| ||   |   |   | || |     | |  |
      GACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTC
      540       550       560       570       580       590       600

   1160      1170      1180      1190      1200         1210      1220
      TTGTCACCGACTCTGACCTCGGCGTTGTAACCGGAGGTGTC---GACCAAGGCGTTCTTCTTGTTCTGCAAG
       | |    ||       |||    ||  |  | ||  ||||   | ||||            || |   |
      ATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATC
    610       620       630       640       650       660       670       680

    1230      1240      1250      1260      1270      1280      1290
      GACAAGATCTTGGAGTCGTTGATGGAGTTGAAGTACTCGTTGATGATGTCCTTCAACAAGGAGT---TGTTG
       |      ||  || |   |||  || ||   |         | |||||| |  |||  |  | |   ||||
      CAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTC
            690       700       710       720       730       740       750

     1300      1310      1320      1330      1340          1350
      GTGTAGGAGAAGATGTTGAATGGCATGGTGTTCTCGAAGGACTC----GTTGACCTTAGCC--------TTC
            |  || | |     |  |||     |   ||| |||||    ||||     | ||        | |
      AATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCC
          760       770       780       790       800       810       820

     1360      1370   X
      AAACGCATCGTGAATTC
      |||  || |  ||| ||
      AAATACAACCAGAACTCTAAATACATCAACTACCGCG
        830       840 X     850       860
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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-12.res made by bobryen on Thu 7 Nov 102 14:33:46-PST.


Query sequence being compared:US-09-910-186A-12 (1-451)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-12 (1-451) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -                                          *        *          *
S    0---------------------------------------------------------------------
      |     ||      |  |   |     ||      |  |   |     ||      |  |   |
SCORE 0     20     39  |  59     79     98  | 118    138    157  | 177
STDEV      -4         -3        -2         -1         0          1


                             PARAMETERS

Similarity matrix       PAM-150     K-tuple                      1
Threshold level of sim.     16%
Mismatch penalty              1     Joining penalty             20
Gap penalty                5.00     Window size                451
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                             SEARCH STATISTICS

Scores:                  Mean       Median     Standard Deviation
                         147          120        29.05

Times:                   CPU                   Total Elapsed
                     00:00:00.00               00:00:00.00

Number of residues:                  1704
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best_scores is:
```

```
                                                       Init. Opt.
Sequence Name     Description                      Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
   1. US-08-123-975A-3 Sequence 3, Application U    415   177   236    1.03    0
                     ****  0 standard deviation from mean ****
   2. US-08-123-975A-2 Sequence 2, Application U    850   145   265   -0.07    0
   3. US-08-123-975A-5 Sequence 5, Application U    439   119   244   -0.96    0


1. US-09-910-186A-12 (1-451)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    177  Optimized Score  =    236  Significance =  1.03
Residue Identity =    26%  Matches          =    109  Mismatches   =   267
Gaps             =      8  Conservative Substitutions              =    28

     30        40        50        60        70        80        90
    LKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNTIYTNDFKL-SSSGDKIIVNLNNNIL
                            | |:| | | : : :|  |    |  |   |      || | | | |
                        RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                        X       10        20        30        40        50

   100       110         120       130       140       150       160
    YSAIYENSSVSFWIKISK--DLTNSHNEYTIINSIEQNSGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESL
    | : ||| | ||||:| |        |||||||  | |||||     | | | |||        :| ||
    YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI
          60        70        80        90       100       110       120

   170       180       190       200       210       220       230       240
    SHTGYTNKWFFVTITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSK
        | |:| ||||||| :   | |||| |     |  |  :     | |  |   |     ||: || | |
    NISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDK
       130       140       150       160       170       180       190

           250       260       270       280       290       300       310
    ELSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLVLVQYPDLSKLYTGNPITI
    ||   :|   |: |    : ||:||  | :|  ||  |     :|:           |    :
    ELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIY
     200       210       220       230       240       250       260

         320            330       340       350       360       370
    KSVSDKNPYSRILN-----GDNIILHMLYNSRKYMIIRDTDTIYATQGGECSQNCVYALKLQSNLGNYGIGI
       |       |           |           :::  :   || :       : :       ||    :
    LNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVV
   270       280       290       300       310       320       330       340

  380       390       400       410       420       430       440       450
    FSIKNIVSKNKYCSQIFSSFRENTMLLADIYKPWRFSFKNAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
                                  :       |           |         | ||  | || |
    VMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGE
           350       360       370       380       390       400       410 X

    RPL


2. US-09-910-186A-12 (1-451)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    145  Optimized Score  =    265  Significance = -0.07
Residue Identity =    30%  Matches          =    147  Mismatches   =   273
Gaps             =     31  Conservative Substitutions              =    25

                        X       10        20        30        40        50
                        MRLKAKVNESFENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKN
                           |:|||      |||    |||   | :  | |   |    || |  | |
    LKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDN
           370       380       390       400       410       420       430

          60        70        80        90       100       110       120
    ALVDTSGYNAEVRVGDNVQLNTIYTNDFKLSSSGDKIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS---
```

```
 |:| ||| | | | | | ||         ||:  || |  | || : :::   ||||||:| |
NLIDLSGYGAKVEVYDGVELNDKNQFKLT-SSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQN
     440       450       460       470       480       490       500

        130       140       150       160       170       180       190
--HNEYTIINSIEQNSGWKLCIRNGNIEWILQDVNRKYKSLIFDYSESLSHTGYTNKWFFVTITNNIMGYMK
  ||||||||    |||||  ||   | | | |:| | ||  |:|        | |:|||||||||  :   |
YIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAK
    510       520       530       540       550       560       570

      200       210       220       230       240       250       260
LYINGELKQSQKIEDLDEVKLDKTIVFGIDENIDENQMLWIRDFNIFSKELSNEDINIVYEGQILRNVIKDY
 |||| |     | |  ||     |:|  |  ||  |  | : | ||  |||   |   |  |      ||:
IYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDF
   580       590       600       610       620       630       640

    270       280       290                  300       310       320
WGNPLKFDTEYYIINDNYIDRYIAPESNVLV-----------LVQYPDLSKLYTGNPITIKSVSDKNPYSRI
||||| :  |||  |      ||       |              |     || |    |:  |
WGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDD
 650       660       670       680       690       700       710

   330                340       350       360       370       380
LNGDNIILHMLY---------NSRKYMIIRDTDTIYATQGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVS
         : :            ||    :     |              |       |       |   |
IVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEES
720       730       740       750       760       770       780       790

390       400       410       420       430       440                 X
KNKYCSQIFSSFRENTMLLADIYKPWRFSFKNAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
           | |      :     :  |  :             |     | || :| || |
TDEIGLIGIHRFYESGIVFEE----YKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
       800      810           820       830       840       850


3. US-09-910-186A-12 (1-451)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =    119  Optimized Score  =     244  Significance = -0.96
Residue Identity  =    30%  Matches          =     136  Mismatches   =   255
Gaps              =     31  Conservative Substitutions                =    23

       20        30 X      40        50        60        70        80
ENTMPFNIFSYTNNSLLKDIINEYFNSINDSKILSLQNKKNALVDTSGYNAEVRVGDNVQLNTIYTNDFKLS
                     | |   |    || |  | | |:| ||| | | | | | ||         |
                    FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLT-S
                    X       10        20        30        40        50

     90       100       110       120            130       140       150
SSGDKIIVNLNNNILYSAIYENSSVSFWIKISKDLTNS-----HNEYTIINSIEQNSGWKLCIRNGNIEWIL
|:  || |  | || : :::   ||||||:| |          ||||||||    |||||  ||   | | |
SANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTL
       60        70        80        90       100       110       120

       160       170       180       190       200       210       220
QDVNRKYKSLIFDYSESLSHTGYTNKWFFVTITNNIMGYMKLYINGELKQSQKIEDLDEVKLDKTIVFGIDE
 |:| | ||  |:|        | |:||||||||| :   | |||| |     | |  ||     |:|  |
IDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG
    130       140       150        160       170       180       190

     230       240       250       260       270       280       290
NIDENQMLWIRDFNIFSKELSNEDINIVYEGQILRNVIKDYWGNPLKFDTEYYIINDNYIDRYIAPESNVLV
 ||  |  | : | ||  |||   |   |  |      ||:||||| :  |||  |      ||       |
DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPV
   200       210       220       230       240       250       260

              300       310       320       330                 340
-----------LVQYPDLSKLYTGNPITIKSVSDKNPYSRILNGDNIILHMLY---------NSRKYMIIRD
              |     || |    |:  |                 : :            ||    :
GEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEE
 270       280       290       300       310       320       330

 350       360       370       380       390       400       410
```

```
TDTIYATQGGECSQNCVYALKLQSNLGNYGIGIFSIKNIVSKNKYCSQIFSSFRENTMLLADIYKPWRFSFK
     |              |       |       |   |           | |      :     :  |
EKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEE----YKDYFC
340       350       360       370       380       390       400

420       430       440       450
NAYTPVAVTNYETKLLSTSSFWKFISRDPGWVE
 :             |     | || :| || |
ISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
 410       420       430       X
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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-13.res made by bobryen on Thu 7 Nov 102 14:44:27-PST.


Query sequence being compared:US-09-910-186A-13 (1-1400)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-13 (1-1400) with:
        File : US08123975A.seq

   100-
      -
 N    -
 U  50-
 M    -
 B    -
 E    -
 R    -
      -
 O    -
 F  10-
      -
 S    -
 E   5-
 Q    -
 U    -
 E    -                                                               *
 N    -
 C    -
 E    -                                                 *
 S   0------------------------------------------------------------------
        |     | |    |    |  |     ||     ||     |    |  |     ||     |
SCORE 0      47 |    95   |142    190    237|    285   |332    380   427
STDEV             -5         -4          -3          -2        -1      0


                          PARAMETERS

Similarity matrix      Unitary     K-tuple                     4
Mismatch penalty             1     Joining penalty            30
Gap penalty               5.00     Window size               500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                       SEARCH STATISTICS

Scores:                 Mean        Median       Standard Deviation
                         392          323          60.62

Times:                  CPU                      Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init.  Opt.
Sequence Name     Description                      Length  Score Score  Sig. Frame
-----------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U    1338    427   692   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U    1338    427   692   0.58    0
              ****  1 standard deviation below mean  ****
   3. US-08-123-975A-6 Sequence 6, Application U    1351    322   612  -1.15    0


1. US-09-910-186A-13 (1-1400)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    427  Optimized Score   =    692  Significance =  0.58
Residue Identity  =    54%  Matches           =    739  Mismatches   =   539
Gaps              =     72  Conservative Substitutions               =     0

    70        80        90       100       110       120       130       140
    TCCTTTTAAGCTTTCTTCTTATACAGATGATAAAATTTTAATTTCCTACTTCAACAAGTTCTTCAAGAGAAT
                         |  ||          | |  | ||   |||||   | | | ||||||  ||
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

           150       160       170       180       190       200       210
    TAAGTCTTCTTCCGTTTTAAACATGAGATACAAGAATGATAAATACGTCGACACTTCCGGTTACGACTCCAA
     |    | ||| |  | || || | ||| |     ||  |     |||||   ||  | ||||  |||||
    CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
          60        70        80        90       100       110       120

         220       230       240       250       260       270       280
    TATCAACATTAACGGTGACGTGTACAAGTACCCAACTAACAAAAACCAATTCGGTATCTACAACGACAAGCT
     ||||||||      | | ||  ||    | || |   |||| || ||  ||    | | |||     |
    AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
       130       140       150       160       170       180       190

       290       300       310       320       330       340       350
    TTCCGAGGTCAACATCTCTCAAAACGACTACATTATCTACGACAACAAGTACAAGAACTTCTCTATTTCTTT
    |||| |  || |  |    |  ||  |    ||  | ||| ||   | |||| | |||||||| |  || ||
    TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTT
     200       210       220       230       240       250       260

     360       370       380       390       400       410       420
    CTGGGTCAGGATTCCTAACTACGACAACAAGATCGTCAACGTTAACAACGAGTACACTATCATCAACTGTAT
    |||| || | || || || ||  ||||     | ||     | ||||| || ||||| ||||||||| ||
    CTGGATCCGTATCCCGAAATACTTCAAC---TCCATCTCTCTGAACAATGAATACACCATCATCAACTGCAT
   270       280       290          300       310       320       330

   430       440       450       460       470       480       490       500
    GAGAGACAACAACTCCGGTTGGAAGGTCTCTCTTAACCACAACGAGATCATTTGGACCTTGCAAGACAACGC
    |   || ||||| || |||||||| || ||||| ||| ||   || ||||| |||||  |||| ||||
    G---GAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCA
       340       350       360       370       380       390       400

           510       520       530       540       550       560       570
    AGGTATTAACCAAAAGTTAGCATTCAACTACGGTAACGCAAACGGTATTTCTGACTACATCAACAAGTGGAT
     |  || || ||     | | |||||| |||  | |    | |   || |||||||||||||    |||||
    GGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGAT
     410       420       430       440       450       460       470

         580       590       600       610       620       630       640
    TTTCGTCACTATCACTAACGACAGATTAGGTGACTCTAAGCTTTACATTAACGGTAACTTAATCGACCAAAA
     ||||| || ||||| ||| |  |  |   | |||| ||  | ||||| |||||     | |||||||| ||
    CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAA
   480       490       500       510       520       530       540       550

       650       660       670       680       690       700       710
    GTCCATTTTAAACTTAGGTAACATTCACGTTTCTGACAACATCTTATTCAAGATCGTTAACTGCAGTTACAC
      | || |  ||  | |||||||| |||| |||| | ||||||| | ||||| |  | |     ||  || ||||
    ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACAC
             560       570       580       590       600       610       620

        720       730       740       750       760       770       780
    ---CAGATACATTGGCATTAGATACTTCAACATTTTCGACAAGGAGTTAGACGAGACCGAGATTCAAACTTT
       | | |||||  | || | |||||||||  | |||||||||| ||  |  |||| |  || ||  ||     |
    TCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCT
         630       640       650       660       670       680       690

      790       800       810       820       830       840       850
    ATACAGCAACGAACCTAACACCAATATTTTGAAGGACTTCTGGGGTAACTACTTGCTTTACGACAAGGAATA
     |||  |||| |  | ||  |   |||  |||| |||||||||||| ||||| |||  ||||||||    ||
    GTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTA
       700       710       720       730       740       750       760

    860       870       880       890           900       910       920
    CTACTTATTAAACGTGTTAAAGCCAAACAACTTCATTGA----TAGGAGAAAGGATTCTACTTTAAGCATTA
    |||| |  | ||  |||   | || ||||| | | ||||     |  |   |||  ||  |  | |    ||
    CTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTA
     770       780       790       800       810       820       830

      930       940       950                   960                 970
    ACAACATCAGAAGCACTATTCTTTT------------AGCTAACAGA--------TTATACTCTGGTATCAA
     |   |      ||    |||| ||            | ||| | ||         | |||  ||||| |||
    CCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAA
   840       850       860       870       880       890       900       910

    980       990      1000      1010      1020      1030      1040
    GGTTAAGATCCAAAGAGTTAACAACTCTTCTACTAACGATAACCTTGTTAGAAAGAACGATCAGGTCTATAT
      | |  ||| | | |    ||   |||  ||  || ||  | ||| | || || ||||  || || ||
    ATTCATCATCAAGAAA---TACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACAT
           920          930       940       950       960       970

 1050      1060          1070      1080        1090      1100      1110
    TAACTTCGTCGCT----AGCAAGACTCACTTATTCCCATTA--TATGCTGATACCGCTACCACCAACAAGGA
     ||  | || | |    |  |||| |  | | |  | |  |    | || |  | | |      || |
    CAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTT
  980       990      1000      1010      1020      1030      1040      1050

     1120      1130      1140      1150      1160      1170
    GAAGACCATCAAGATCTCCTCCTCTGGCAACAGATTTAACCAAGTCGTCGTTATGAACTCC-----------
    |    |  |  | ||| |   |  ||| ||    | |   || || || || ||||| |||
    GTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCT---CAGGTAGTTGTAATGAAATCCAAGAACGACCA
         1060      1070      1080         1090      1100      1110      1120

        1180      1190      1200      1210      1220      1230      1240
    ----GTCGGTAACAACTGTACCATGAACTTTAAAAATAATAATGGAAATAATATTGGGTTGTTAGGTTT---
         ||  |||||| || |  |||||  |  |  | || ||||| ||  |||| || ||  | |||||
    GGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCA
          1130      1140      1150      1160      1170      1180      1190

                  1250      1260      1270      1280      1290      1300
    ---------CAAGGCAGATACTGTAGTTGCTAGTACTTGGTATTATACCCACATGAGAGATCACACCAACAG
             |||    | ||   | ||||||   |  |||||  ||   || ||   |  |  | |   ||
    CCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCAC
        1200      1210      1220      1230      1240      1250      1260

      1310      1320      1330      1340      1350      1360      1370
    CAATGGATGTTTTTGGAACTTTATTTCTGAAGAACATGGATGGCAAGAAAAATAATAGGGATCCGCGGCCGC
        || || | |||| | || ||  | |  ||  | || |||   |||        |  | ||| |   ||
    TCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGC
      1270      1280      1290      1300      1310      1320      1330

    1380      1390
    ACGCGTCCCGGGACTAGTGAAT

    TT
     X


2. US-09-910-186A-13 (1-1400)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    427  Optimized Score  =       692  Significance =  0.58
Residue Identity =    54%  Matches          =       739  Mismatches   =   539
Gaps             =     72  Conservative Substitutions              =     0

    70        80        90       100       110       120       130       140
    TCCTTTTAAGCTTTCTTCTTATACAGATGATAAAATTTTAATTTCCTACTTCAACAAGTTCTTCAAGAGAAT
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                         |  ||          | |  | ||   |||||   | | | ||||||  ||
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

           150       160       170       180       190       200       210
    TAAGTCTTCTTCCGTTTTAAACATGAGATACAAGAATGATAAATACGTCGACACTTCCGGTTACGACTCCAA
     |    | | ||| |  | ||| || | ||| |     || |     |||||   ||  | ||||  |||||
    CATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAA
          60        70        80        90       100       110       120

         220       230       240       250       260       270       280
    TATCAACATTAACGGTGACGTGTACAAGTACCCAACTAACAAAAACCAATTCGGTATCTACAACGACAAGCT
     ||||||||      | | ||  ||    | || |   |||| || ||  ||    | | |||     |
    AATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATC
       130       140       150       160       170       180       190

       290       300       310       320       330       340       350
    TTCCGAGGTCAACATCTCTCAAAACGACTACATTATCTACGACAACAAGTACAAGAACTTCTCTATTTCTTT
    |||| |  || |  |    |  ||  |    ||  | ||| ||   | |||| | |||||||| |  || ||
    TTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTT
     200       210       220       230       240       250       260

     360       370       380       390       400       410       420
    CTGGGTCAGGATTCCTAACTACGACAACAAGATCGTCAACGTTAACAACGAGTACACTATCATCAACTGTAT
    |||| || | || || |||  ||||     | ||    | ||||| || ||||| ||||||||||| ||
    CTGGATCCGTATCCCGAAATACTTCAAC---TCCATCTCTCTGAACAATGAATACACCATCATCAACTGCAT
   270       280       290          300       310       320       330

   430       440       450       460       470       480       490       500
    GAGAGACAACAACTCCGGTTGGAAGGTCTCTCTTAACCACAACGAGATCATTTGGACCTTGCAAGACAACGC
    |   || ||||| || |||||||| || ||||| ||| ||   || ||||| |||||  |||| ||||
    G---GAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCA
       340       350       360       370       380       390       400

           510       520       530       540       550       560       570
    AGGTATTAACCAAAAGTTAGCATTCAACTACGGTAACGCAAACGGTATTTCTGACTACATCAACAAGTGGAT
     |  || || ||     | | |||||| |||  | |    | |   || ||||||||||||||    |||||
    GGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGAT
     410       420       430       440       450       460       470

         580       590       600       610       620       630       640
    TTTCGTCACTATCACTAACGACAGATTAGGTGACTCTAAGCTTTACATTAACGGTAACTTAATCGACCAAAA
     ||||| || ||||| ||| |  |  |   | |||| ||  | ||||| |||||     | |||||||| ||
    CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAA
   480       490       500       510       520       530       540       550

       650       660       670       680       690       700       710
    GTCCATTTTAAACTTAGGTAACATTCACGTTTCTGACAACATCTTATTCAAGATCGTTAACTGCAGTTACAC
      | || |  ||  | |||||||| |||| |||| | |||||| | |||||  | |     ||  || ||||
    ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACAC
           560       570       580       590       600       610       620

        720       730       740       750       760       770       780
    ---CAGATACATTGGCATTAGATACTTCAACATTTTCGACAAGGAGTTAGACGAGACCGAGATTCAAACTTT
       | | |||||  | || | |||||||||  | |||||||| ||  |  |||| |  || ||  ||    |
    TCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCT
         630       640       650       660       670       680       690

      790       800       810       820       830       840       850
    ATACAGCAACGAACCTAACACCAATATTTTGAAGGACTTCTGGGGTAACTACTTGCTTTACGACAAGGAATA
     |||  |||| |  | ||  |   |||  |||| |||||||||||| ||||| |||  ||||||||    ||
    GTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTA
       700       710       720       730       740       750       760

    860       870       880       890           900       910       920
    CTACTTATTAAACGTGTTAAAGCCAAACAACTTCATTGA----TAGGAGAAAGGATTCTACTTTAAGCATTA
    |||| |  | ||  |||   | || ||||| | | ||||     |  |   |||  ||  |  | |    ||
    CTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTA
     770       780       790       800       810       820       830

      930       940       950                   960                 970
    ACAACATCAGAAGCACTATTCTTTT------------AGCTAACAGA--------TTATACTCTGGTATCAA
     |   |      ||    |||| ||            | ||| | ||         | |||  ||||| |||
    CCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAA
   840       850       860       870       880       890       900       910

    980       990      1000      1010      1020      1030      1040
    GGTTAAGATCCAAAGAGTTAACAACTCTTCTACTAACGATAACCTTGTTAGAAAGAACGATCAGGTCTATAT
      | |  ||| | | |    ||   |||  ||  || || ||  | ||| | || || ||||  || || ||
    ATTCATCATCAAGAAA---TACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACAT
           920          930       940       950       960       970

 1050      1060          1070      1080        1090      1100      1110
    TAACTTCGTCGCT----AGCAAGACTCACTTATTCCCATTA--TATGCTGATACCGCTACCACCAACAAGGA
     ||  | || | |    |  |||| |  | | |  | |  |    | || |  | | |      || |
    CAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTT
  980       990     1000      1010      1020      1030      1040      1050

     1120      1130      1140      1150      1160      1170
    GAAGACCATCAAGATCTCCTCCTCTGGCAACAGATTTAACCAAGTCGTCGTTATGAACTCC-----------
    |    |  |  | ||| |   |  ||| ||    | |   || || || || ||||| |||
    GTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCT---CAGGTAGTTGTAATGAAATCCAAGAACGACCA
         1060      1070      1080         1090      1100      1110      1120

        1180      1190      1200      1210      1220      1230      1240
    ----GTCGGTAACAACTGTACCATGAACTTTAAAAATAATAATGGAAATAATATTGGGTTGTTAGGTTT---
         ||  |||||| || |  |||||  |  |  | || |||||  ||  |||| || ||  | |||||
    GGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCA
          1130      1140      1150      1160      1170      1180      1190

                  1250      1260      1270      1280      1290      1300
    ---------CAAGGCAGATACTGTAGTTGCTAGTACTTGGTATTATACCCACATGAGAGATCACACCAACAG
             |||    | ||   | ||||||   |  |||||  ||   || ||   |  |  | |   ||
    CCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCAC
        1200      1210      1220      1230      1240      1250      1260

      1310      1320      1330      1340      1350      1360      1370
    CAATGGATGTTTTTGGAACTTTATTTCTGAAGAACATGGATGGCAAGAAAAATAATAGGGATCCGCGGCCGC
        || || | |||| | || ||  | |  ||  | || |||   |||        |  | ||| |   ||
    TCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGC
      1270      1280      1290      1300      1310      1320      1330

    1380      1390
    ACGCGTCCCGGGACTAGTGAAT

    TT
     X


3. US-09-910-186A-13 (1-1400)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    322  Optimized Score  =    612  Significance = -1.15
Residue Identity =    50%  Matches          =    682  Mismatches   =   585
Gaps             =     88  Conservative Substitutions          =     0

          100       110 X     120       130       140       150       160
    CAGATGATAAAATTTTAATTTCCTACTTCAACAAGTTCTTCAAGAGAATTAAGTCTTCTTCCGTTTTAAACA
                              |||||||| | |        |||   |     |  | |  | |||
                            ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X      10        20        30        40        50

        170       180       190       200       210       220       230
    TGAGATACAAGAATGATAAATACGTCGACACTTCCGGTTACGACTCCAATATCAACATTAACGGTGACGTGT
    || | |||||  |  | ||     ||||    || |||||||   | ||  |  |  |  |||  |  ||||
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACG--GTGT
          60        70        80        90       100       110         120

      240       250       260       270       280       290       300
    ACAAGTACCCAACTAACAAAAACCAATTCGGTATCTACAACGACAAGCTTTCCGAGGTCAACATCTCTCAAA
      || |     | | |||| ||||| |||    |   |     |      ||  || ||    |  |||| |
    TGAACT----GAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGA
             130       140       150       160       170       180       190

    310       320       330       340       350       360       370
    ACGACTACATTATCTACGACAACAAGTACAAGAACTTCTCTATTTCTTTCTGGGTCAGGATTCCTAACTACG
    |  |  |||| |||| | ||  |   | |  | ||||||||| |||| |||||| || | || || || |||
    ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
           200       210       220       230       240       250       260

  380       390             400       410       420       430       440
    ACAACAAGATCGTC------AACGTTAACAACGAGTACACTATCATCAACTGTATGAGAGACAACAACTCCG
    | ||| |     ||       || |  ||||| || ||||| ||||||||||| ||||   | || ||||| |
    AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGA---AGAATAACTCTG
         270       280       290       300       310          320       330

      450       460       470       480       490       500       510
    GTTGGAAGGTCTCTCTTAACCACAACGAGATCATTTGGACCTTGCAAGACAACGCAGGTATTAACCAAAAGT
    |||||||| ||||  |   |   |||   ||||| |||||  ||   || | |   ||||  | | ||
    GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTG
          340       350       360       370       380       390       400

    520       530       540       550       560       570       580
    TAGCATTCAACTACGGTAACGCAAACGGTATTTCTGACTACATCAACAAGTGGATTTTCGTCACTATCACTA
    ||   ||| | |||   | |    | |  || ||||| ||||||||    ||| | ||||| || ||||| |
    TATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCA
        410       420       430       440       450       460       470

  590       600       610       620       630       640       650       660
    ACGACAGATTAGGTGACTCTAAGCTTTACATTAACGGTAACTTAATCGACCAAAAGTCCATTTTAAACTTAG
    |  ||    |     |  ||||  | ||||| ||||||||  |        | |    |||   | || |
    ATAAC---CTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCC
      480          490       500       510       520       530       540

          670       680       690          700       710       720       730
    GTAACATTCACGTTTCTGACAACATCTTATTCAA---GATCGTTAACTGCAGTTACACCAGATACATTGGCA
    || |  ||  || |   |   | ||| | |||||   |  || | ||  |   |||   | |||  | |
    GTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
       550       560       570       580       590       600       610

           740       750       760       770       780       790       800
    TTAGATACTTCAACATTTTCGACAAGGAGTTAGACGAGACCGAGATTCAAACTTTATACAGCAACGAACCTA
    | | |||||||  ||| ||| |||  ||  |     || || | ||  ||      ||||  | | |  ||
    TGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTT
     620       630       640       650       660       670       680

         810       820       830       840       850       860       870
    ACACCAATATTTTGAAGGACTTCTGGGGTAACTACTTGCTTTACGACAAGGAATACTACTTATTAAACGTGT
    || || |     |||| ||||||||||||||     || | ||| |||| ||||||||  | || || |
    ACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTG
   690       700       710       720       730       740       750       760

       880       890       900       910                    920       930
    TAAAGCCAAACAACTTCATTGATAGGAGAAAGGATTCT-------------ACTTTAAGCATTAACAACATC
      ||    |||   | |||  |   ||  || || |||              | | |  | ||   || |
    GTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACA
           770       780       790       800       810       820       830

        940       950            960       970       980       990      1000
    AGAAGCACTATTCTTTTAGCTA-----ACAGATTATACTCTGGTATCAAGGTTAAGATCCAAAGAGTTAACA
    |  || ||| |   |  | | |      |    | |||   |||   ||| | |  ||||   |       |
    ACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTA
         840       850       860       870       880       890       900

             1010      1020      1030      1040      1050      1060
    ACTCT---TCTACTAACGATAACCTTGTTAGAAAGAACGATCAGGTCTATATTAACTTCGTCGCTAGCAAGA
    |||||   || |  || ||| || | ||  | ||  | ||  |  ||||  |  ||||| ||   | |  ||
    ACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTC---AACCTGA
       910       920       930       940       950       960          970

 1070      1080      1090      1100      1110      1120                 1130
    CTCACTTATTCCCATTATATGCTGATACCGCTACCACCAACAAGGAGAAGACCATC-----------AAGAT
     |||   ||  |   | ||| |   |||   |||  | |  ||| ||||||  | |             |||
    ATCAGGAATGGC--GTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGAT
        980         990      1000      1010      1020      1030      1040

          1140      1150      1160      1170      1180            1190
    CTCCTCCTCTGGCAACAGATTTAACCAAGTCGTCGTTATGAACTCCGTCG------GTAACAACTGTACCAT
    |||    || | | |    |  |||    ||    | |   | | || ||        | | ||| |  |
   CTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCA
      1050      1060      1070      1080      1090      1100      1110

   1200      1210      1220      1230      1240      1250      1260
   GAACTTTAAAAATAATAATGGAAATAATATTGGGTTGTTAGGTTTCA-AGGCAGATACTGTAGTTGCTAGTA
   |    |    || ||  ||| | |   || ||      | ||| | |  || |   || ||   | | | |
   GCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATC
    1120      1130      1140      1150      1160      1170      1180

  1270      1280        1290      1300          1310      1320      1330
   CTTGGTATTATACCCACA--TGAGAGATCACACCAACAGC----AATGGATGTTTTTGGAACTTTATTTCTG
        |  ||| |  | |    | |||  ||  |  || |    |||||    |   |||| || |   |
   TGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAA
  1190      1200      1210      1220      1230      1240      1250

                1340      1350        1360      1370      1380      1390
   A----------AGAACATGGATGGCAA--GAAAAATAATAGGGATCCGCGGCCGCACGCGTCCCGGGACTAG
   |           |||  ||| | ||||  |  |  | ||   ||    ||     | |  |     || |||
   ACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACG-----AAGGTTGGACCGAATAG
1260      1270      1280      1290      1300           1310      1320

      1400
   TGAATTC
   | |  ||
   TAACCTCTAGAGTCGAGGCCTGCAG
   1330  X   1340      1350
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-13-inv.res made by bobryen on Thu 7 Nov 102 14:44:44-PST.


Query sequence being compared:US-09-910-186A-13' (1-1400)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-13' (1-1400) with:
        File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                              *
N     -
C     -
E     -                                            *
S    0--------------------------------------------------------------------
      |      |  |   |     ||      |  |   |      |      |  |   |      |
SCORE 0      5  |   9     14     19  |  23     28     33  |  37     42
STDEV          -4        -3          -2          -1         0


                              PARAMETERS -

Similarity matrix      Unitary    K-tuple                       4
Mismatch penalty             1    Joining penalty              30
Gap penalty               5.00    Window size                 500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                   Mean        Median      Standard Deviation
                            38            31            6.93

Times:                  CPU                       Total Elapsed
                    00:00:00.00                   00:00:00.00

Number of residues:                   4027
Number of sequences searched:            3
Number of scores above cutoff:           3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                      Length Score Score  Sig. Frame
----------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U    1338    42   273   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U    1338    42   273   0.58    0
                 ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U    1351    30   480  -1.15    0

1. US-09-910-186A-13' (1-1400)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     42  Optimized Score =    273  Significance =  0.58
Residue Identity  =    42%  Matches         =    333  Mismatches   =   384
Gaps              =     68  Conservative Substitutions             =     0

                        X       10        20        30            40
                        GAATTCACTAGTCCCGGGACGCGTGCGGCCGC----GGATCCCTATTATTTT
                         | |  ||   |  || ||| |   | ||  |    |||||       |
    TTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAA
           590       600       610       620       630       640       650

    50        60        70        80                 90        100       110
    TCTTGCCATCCATGTTCTTCAGAAATAAAGTTCCAAA---------AACATCCATTGCTGTTGGTGTGATCT
    |||   |  | | |  ||  |  || ||     ||||          ||| ||| | |  ||   ||   ||
    TCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCT
         660       670       680       690       700       710       720

              120       130         140       150       160       170
    ----CTCATGTGGGTATAATACC--AAGTACTAGCAACTACAGTATCTGCCTTGAAACCTAACAACCCAATA
          | | ||||   | ||||   ||||| |  |||   | ||  |||  |||| |   || | || |
    GAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGC--TGAATCTGTACGATCCGAAC
       730       740       750       760       770         780       790

    180       190       200       210       220       230       240
    TTATTTCCATTATTATTTTTAAAGTTCATGGTACAGTTGTTACCGACGGAGTTCATAACGACGACTTGGTTA
      ||    |   | |  |  | | |  | |   | |  |||||  | | |  | | || | |  | ||||
    AAAT----ACGTTGACGTCAACAATGTAGGTATCCGCGGTTAC--ATGTACCTGA-AAGGTCCGCGTGGT--
           800       810       820       830         840        850

  250       260       270       280       290        300       310       320
    AATCTGTTGCCAGAGGAGGAGATCTTGATGGTCTTCTCCTTGT-TGGTGGTAGCGGTATCAGCATATAATGG
      ||||||   |       | ||||   ||  ||  ||| |||   |||||| |    ||| |||  |   |
    --TCTGTTATGA-CTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAA---G
      860        870       880       890       900       910       920

           330       340       350       360       370       380       390
    GAATAAGTGAGTCTTGCTAGCGACGAAGTTAATATAGACCTGATCGTTCTTTCTAACAAGGTTATCGTTAGT
     |||| | |  |               | ||| |  |||   |||||||     ||  |   | |    |
    AAATACGCGTCT---------------GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATC
        930                      940       950       960       970       980

         400       410       420       430       440       450       460
    AGAAGAGTTGTTAACTCTTTGGATCTTAACCTTGATACCAGAGTATAATCTGTTAGCTAAAAGAATAGTGCT
    |     || |||||       ||       || | |||||  |  |     | | |   | | || |
    AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTG
           990      1000      1010      1020      1030      1040      1050

       470       480       490       500       510       520       530
    TCTGATGTTGTTAATGCTTAAAGTAGAATCCTTTCTCCTATCAATGAAGTTGTTTGGCTTTAACACGTTTAA
    |||| | | |  |   |  |   | | |  || ||||          || |  |||   | ||  |    ||
    TCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTC----------AGGTAGTTGTAATGAAATCCAAGAA
        1060      1070      1080                1090      1100      1110

     540       550       560       570       580       590       600
    TAAGTAGTATTCCTTGTCGTAAAGCAAGTAGTTACCCCAGAAGTCCTTCAAAATATTGGTGTTAGGTTCGTT
      |  ||  |  |       || ||||  | | |  |   | | |    |   ||  | | |  | ||| |
    CGACCAGGGTATCACTAACAAATGCAA--AATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATC
      1120      1130      1140        1150      1160      1170      1180

   610       620       630       640        650       660       670
    GCTGTATAAAGTTTGAATCTCGGTCTCGTCTAACTCCTTG-TCGAAAATGTTGAAGTATCTAATGCCAATGT
    | | |  |    || ||   |  | |||   ||||  ||| |   || || |  | |    |   | || ||
  GGTTTCCACCAGTTCAA---CAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGT
    1190      1200         1210      1220      1230      1240      1250

680       690       700       710       720       730       740       750
  ATCTGGTGTAACTGCAGTTAACGATCTTGAATAAGATGTTGTCAGAAACGTGAATGTTACCTAAGTTTAAAA
    ||   | |      |||     |      | |       | |  |  ||    || | |      |  ||
  TCCTCTCGCACTCTGGGTTGCTCTTGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
     1260      1270      1280      1290      1300      1310      1320

        760   X   770       780
  TGGACTTTTGGTCGATTAAGTTACCGTTAATGT
           | |
  CCCGGGAAAGCTT
   1330       X


2. US-09-910-186A-13' (1-1400)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     42  Optimized Score  =    273  Significance =  0.58
Residue Identity =     42%  Matches          =    333  Mismatches   =   384
Gaps             =     68  Conservative Substitutions             =     0

                      X       10        20        30            40
                      GAATTCACTAGTCCCGGGACGCGTGCGGCCGC----GGATCCCTATTATTTT
                       | |  ||   |  || ||| |   | ||  |    |||||       |
  TTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAA
         590     600       610       620       630       640       650

  50        60        70        80                 90       100       110
  TCTTGCCATCCATGTTCTTCAGAAATAAAGTTCCAAA---------AACATCCATTGCTGTTGGTGTGATCT
  |||   |  | | |  ||  |  || ||     ||||          ||| ||| | |  ||   ||   ||
  TCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCT
       660       670       680       690       700       710       720

            120       130         140       150       160       170
  ----CTCATGTGGGTATAATACC--AAGTACTAGCAACTACAGTATCTGCCTTGAAACCTAACAACCCAATA
        | | ||||   | ||||   ||||| |  |||   | ||  |||  |||| |   || | || |
  GAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGC--TGAATCTGTACGATCCGAAC
     730       740       750       760       770         780       790

  180       190       200       210       220       230       240
  TTATTTCCATTATTATTTTTAAAGTTCATGGTACAGTTGTTACCGACGGAGTTCATAACGACGACTTGGTTA
    ||    |   | |  |  | | |  | |   | |  |||||  | | |  | | || | |  | ||||
  AAAT----ACGTTGACGTCAACAATGTAGGTATCCGCGGTTAC--ATGTACCTGA-AAGGTCCGCGTGGT--
         800       810       820       830         840        850

250       260       270       280       290        300       310       320
  AATCTGTTGCCAGAGGAGGAGATCTTGATGGTCTTCTCCTTGT-TGGTGGTAGCGGTATCAGCATATAATGG
    ||||||   |       | ||||   ||  ||  ||| |||   |||||| |    ||| |||  |   |
  --TCTGTTATGA-CTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAA---G
    860        870       880       890       900       910       920

         330       340       350       360       370       380       390
  GAATAAGTGAGTCTTGCTAGCGACGAAGTTAATATAGACCTGATCGTTCTTTCTAACAAGGTTATCGTTAGT
   |||| | |  |               | ||| |  |||   |||||||     ||  |   | |    |
  AAATACGCGTCT---------------GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATC
      930                    940       950       960       970       980

       400       410       420       430       440       450       460
  AGAAGAGTTGTTAACTCTTTGGATCTTAACCTTGATACCAGAGTATAATCTGTTAGCTAAAAGAATAGTGCT
  |     || |||||       ||       || | |||||  |  |     | | |   | | || |
  AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTG
         990      1000      1010      1020      1030      1040      1050

     470       480       490       500       510       520       530
  TCTGATGTTGTTAATGCTTAAAGTAGAATCCTTTCTCCTATCAATGAAGTTGTTTGGCTTTAACACGTTTAA
  |||| | | |  |   |  |   | | |  || ||||          || |  |||   | ||  |    ||
  TCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTC----------AGGTAGTTGTAATGAAATCCAAGAA
      1060      1070      1080                1090      1100      1110

   540       550       560       570       580       590       600
  TAAGTAGTATTCCTTGTCGTAAAGCAAGTAGTTACCCCAGAAGTCCTTCAAAATATTGGTGTTAGGTTCGTT

    |  ||  |  |       || |||| | | |  |   | | |    |   ||  | | |  | ||| |
  CGACCAGGGTATCACTAACAAATGCAA--AATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATC
    1120      1130      1140        1150      1160      1170      1180

 610       620       630       640        650       660       670
  GCTGTATAAAGTTTGAATCTCGGTCTCGTCTAACTCCTTG-TCGAAAATGTTGAAGTATCTAATGCCAATGT
  | | |  |    || ||   |  | |||   ||||  ||| |   || || |  | |    |   | || ||
  GGTTTCCACCAGTTCAA---CAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGT
    1190      1200         1210      1220      1230      1240      1250

680       690       700       710       720       730       740       750
  ATCTGGTGTAACTGCAGTTAACGATCTTGAATAAGATGTTGTCAGAAACGTGAATGTTACCTAAGTTTAAAA
    ||   | |      |||     |      | |       | |  |  ||    || | |      |  ||
  TCCTCTCGCACTCTGGGTTGCTCTTGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
     1260      1270      1280      1290      1300      1310      1320

        760   X   770       780
  TGGACTTTTGGTCGATTAAGTTACCGTTAATGT
           | |
  CCCGGGAAAGCTT
   1330       X


3. US-09-910-186A-13' (1-1400)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     30  Optimized Score  =    480  Significance = -1.15
Residue Identity =     41%  Matches          =    572  Mismatches   =   715
Gaps             =    101  Conservative Substitutions             =     0

  40        50        60        70        80        90       100      110
  CTATTATTTTTCTTGCCATCCATGTTCTTCAGAAATAAAGTTCCAAAAACATCCATTGCTGTTGGTGTGATC
                         | | |  | ||||| | |||| ||| | |  |          | | |||
                      ATGGCTTTCAACAAATACAATTCCGAAATCCTGAA-------CAATATCATC
                      X       10        20        30               40

         120       130       140       150       160        170       180
  TCTCATGTGGGTATAATACCAAGTACTAGCAACTACAGTATCTGCCTTGAAAC-CTAACAACCCAATATTAT
      |  || ||    ||| ||| || |  | ||     ||||| || |  ||  |   ||      | |||
  CTGAACCTGCGT----TACAAAG-ACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTAT
     50             60         70        80        90       100       110

        190       200       210       220       230       240       250
  TTCCATTATTATTTTTAAAGTTCATGGTACAGTTGTTACCGACGGAGTTCATAACGACGACTTGGTTAAATC
           |     | ||   || |   |||||   || |||    | |    | |  ||   | |   |
  ACGACGGTGTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCC---GCTAACTCTAAGATCCGTG
       120       130       140       150       160          170       180

      260       270       280       290       300                    310
  TGTTGCCAGAGGAGGAGATCTTGATGGTCTTCTCCTTGTTGGTGGTAGCGGTATC-------------AGCA
  |    |   |  || | ||| |  |   || |   ||  |||   |  | || ||             | |
  TTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCC
        190       200       210       220       230       240       250

       320       330       340       350       360       370       380
  TATAATGGGAATAAGTGAGTCTTGCTAGCGACGAAGTTAATATAGACCTGATCGTTCTTTCTAACAAGGTTA
     |||   |  | |   || |    |   ||      |||  | ||   ||| |    |  |  |||  ||
  CGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATA
      260       270       280       290       300       310       320

     390       400       410       420       430           440       450
  TCGTTAGTAGAAGAGTTGTTAACTCTTTGGATCTTAACCTTGATAC----CAGAGTATAATCTGTTAGCTAA
   |  | || | |   |    | |       | | || | |    ||         ||| | | || ||   |
  ACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCA
    330       340       350       360       370       380       390

       460       470       480       490       500       510       520
  AAGAATAGTGCTTCTGATGTTGTTAATGCTTAAAGTAGAATCCTTTCTCCTATCAATGAAGTTGTTTGGCTT
  ||      | ||||  ||         |   | |      |   | |  | |||  ||  ||| || |
  AATCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTG--GTTCTTCGTTAC
  400       410       420       430       440       450         460

     530       540       550       560       570       580       590
   TAACACGTTTAATAAGTAGTATTCCTTGTCGTAAAGCAAGTAGTTACCCCAGAAGTCCTTCAAAATATTGGT
    | |||   |||   | |  || |       || | |||      ||   |         | | ||    |
   CATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGA
   470       480       490       500       510       520       530

    600       610       620       630       640       650       660
   GTTAGGTTCGTTGCTGTATAAAGTTTGAATCTCGGTCTCGTCTAACTCCTTGTCGAAAATGTTGAAGTATCT
     |  ||    |  |   ||| | |  ||||      || || ||||    |  || |  | |   ||| |
   CATCCGTGAAGTTATCGCTAACGGTGAAATC-----ATCTTCAAACTGGACGGTGACATCGAT--CGTACC-
 540       550       560       570            580       590         600

  670       680       690       700       710       720       730       740
   AATGCCAATGTATCTGGTGTAACTGCAGTTAACGATCTTGAATAAGATGTTGTCAGAAACGTGAATGTTACC
        || |  ||||||   || |  | ||  | ||||| || |      ||||  |  |    ||   |
   -----CAGTTCATCTGGATGAAAT--ACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGA
            610       620         630       640       650       660

          750       760        770                        780       790
   TAAGTTTAAAATGGACTTTTGGT-CGATTAAGTTA-----------------CCGTTAATGTAAAGCTTAGA
      ||  || ||  | | ||  | ||| ||  | |                 ||| | ||||| | |  |||
   ACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGA
  670       680       690       700       710       720       730       740

      800       810       820       830         840       850       860
   GTCACCTAATCTGTCGTTAGTGATAGTGACGAAAATCC--ACTTGTTGATGTAGTCAGAAATACCGTTTGCG
         || | | |  | || | || || | ||  |  || |     || ||  |||    ||| |||
   -----ATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTG--
               750       760       770       780       790       800

      870       880       890       900        910       920       930
   TTACCGTAGTTGAATGCTAACTTTTGGTTAATACCTGC-GTTGTCTTGCAAGGTCCAAATGATCTCGTTGTG
           ||  ||| || |||  |    |||||   | |   |||    |  || |      |    |||
   --------GTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTA
             810       820       830       840       850       860

     940       950         960         970       980       990      1000
   GTTAAGAGAGACCTTC--CAACCGGAGTTGTTGT--CTCTCATACAGTTGATGATAGTGTACTCGTTGTTAA
     |  | || |  |||  || |||  |    | |  ||||||  |  |  ||||   ||   ||||   |||
   CATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGA---TGACATCGTACGTAA
 870       880       890       900       910       920          930

      1010      1020      1030      1040      1050      1060      1070
   CGTTGACGATCTTGTTGTCGTAGTTAGGAATCCTGACCCAGAAAGAAATAGAGAAGTTCTTGTACTTGTTGT
    |  ||| | | | |    | || |    | |||||  ||| ||      |   |   ||   | |  ||
   AGAAGACTA-CATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCA
  940        950       960       970       980       990      1000

    1080      1090      1100      1110      1120      1130      1140
   CGTAGATAATGTAGTCGTTTTGAGAGATGTTGACCTCGGAAAGCTTGTCGTTGTAGATACCGAATTGGTTTT
    | |   |    |   | |||    |     || ||| ||   |       | |  |   | |    ||
   AGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCA
1010      1020      1030      1040      1050      1060      1070      1080

  1150      1160      1170      1180      1190      1200       1210
   TGTTAGTTGGGTACTTGTACACGTCACCGTTAATGTTGATATTGGAGTCGTAACCGGAA-GTGTCGACGTAT
       |   |   |   |   || |   | |    | || | ||  ||    |    |||  |   |||| |
   AAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAA
        1090      1100      1110      1120      1130      1140      1150

 1220      1230      1240      1250      1260      1270      1280      1290
   TTATCATTCTTGTATCTCATGTTTAAAACGGAAGAAGACTTAATTCTCTTGAAGAACTTGTTGAAGTAGGAA
   |     |  | |     ||   ||   ||| |    |  |    |     ||| |    |   |  |  | |
   TCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCA
      1160      1170      1180      1190      1200      1210      1220

         1300      1310       1320      1330      1340      1350      1360
   ATTAAAATTTTATCATCTGTATAAGAAG-AAAGCTTAAAAGGAATACTATTATTTAGGGTATCAGTTACCAT
     |  ||    ||  |   |  | ||||  || |  |||  | | |   | |    ||||  || ||  ||
   TCTCCAA----ATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAG
    1230          1240      1250      1260      1270      1280      1290

        1370       1380      1390      1400
   AGAATTTAG-TTCTTGCTGACTCTCTCCCATGGTGAATTC
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   ||   |      |  |  |    |  || || |  ||
TTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCCTGCAG
   1300      1310      1320      1330  X   1340      1350
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-14.res made by bobryen on Thu 7 Nov 102 14:34:07-PST.

Query sequence being compared:US-09-910-186A-14 (1-449)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

      Results of the initial comparison of US-09-910-186A-14 (1-449) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                            *
N     -
C     -
E     -                                                      *
S    0-------------------------------------------------------------------
      |      |      |     |      ||   | ||  |  ||  | ||   | ||  |  |
SCORE 0     18     35    53     70|   |88|  |105|  123|   140|  |158
STDEV                            -9  -8 -7 -6  -5 -4 -3  -2 -1  0


                         PARAMETERS

Similarity matrix         PAM-150     K-tuple                   1
Threshold level of sim.     16%
Mismatch penalty             1        Joining penalty          20
Gap penalty                5.00       Window size             449
Gap size penalty           0.05
Cutoff score                 1
Randomization group          0

                       SEARCH STATISTICS

Scores:               Mean      Median     Standard Deviation
                       153       144           8.66

Times:                 CPU                   Total Elapsed
                  00:00:00.00                00:00:00.00

Number of residues:                     1704
Number of sequences searched:              3
Number of scores above cutoff:             3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                                Init. Opt.
Sequence Name      Description                           Length Score Score  Sig. Frame
---------------------------------------------------------------------------------------
     1. US-08-123-975A-5 Sequence 5, Application U        439   158   247    0.58   0
     2. US-08-123-975A-2 Sequence 2, Application U        850   158   271    0.58   0
                   **** 1 standard deviation below mean ****
     3. US-08-123-975A-3 Sequence 3, Application U        415   143   276   -1.15   0

1. US-09-910-186A-14 (1-449)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =    158  Optimized Score  =     247  Significance =  0.58
Residue Identity  =    31%  Matches          =     141  Mismatches   =   233
Gaps              =     35  Conservative Substitutions               =    34

      20        30      X 40        50        60        70        80
    NNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIY
                        |||:   |    :||:|||    :| ||| : : :   |      ||||
                        FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGV--ELNDKNQFKLT
                        X       10        20        30          40        50

    90       100       110       120         130       140       150
    NDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYDNKIVN--VNNEYTIINCMRDNNSGWKVSLNHNEIIW
        | : : ||  ||:   :  ||:|||:||| | |  :   : |||||||||: ||||||:|   | |||
    SSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIW
            60        70        80        90       100        110       120

   160       170       180       190       200       210       220       230
    TLQDNAGINQKLAFNYGNANGISDYINKWIFVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKI
    || |  |      | |     ||:|||:| ||||||  |  :| |||| |     |     :     | ||
    TLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKL
          130       140       150        160       170       180       190

            240       250       260       270       280       290       300
    -VNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDS
          | :|  :|| ||  ||    |   |        ||||||| |:| ||||: |    | :|  :|||
    DGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDS
         200       210       220       230       240       250       260

          310       320              330       340       350       360
    TLSINNIRSTILLANRLYSGIKVKI-------QRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATT
           ||      :        |        : |  | ||  ||| | :|  |
    PVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKK
       270       280       290       300       310       320       330

     370            380       390       400       410       420
    NKEKTIKISSSG-----NRFNQVVVMNSVGNNCTMNFKNNNGNNIGLLGFKADTVVASTWYYTHMRD-----
      ||      |      |              | : ||                   |   :   :|
    EEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCIS
     340       350       360       370       380       390       400

              430       440       X
    -----------HTNSNGCFWNFISEEHGWQEK
                    || | ||  : || |
    KWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
   410       420       430        X

2. US-09-910-186A-14 (1-449)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    158  Optimized Score  =     271  Significance =  0.58
Residue Identity  =    32%  Matches          =     155  Mismatches   =   254
Gaps              =     35  Conservative Substitutions               =    35

                        X       10        20        30        40        50
                        MGESQQELNSMVTDTLNNSIPFKLSSYTDDKILISYFNKFFKRIKSSSVLNM
                        :  |     | |   |    || || || | |||  |||:   |    :||:
    DFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNL
      360       370     X 380       390       400       410       420
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          60        70        80        90       100       110       120
    RYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIYNDKLSEVNISQNDYIIYDNKYKNFSISFWVRIPNYD
    |||    :| ||| : : :   |      ||||       | : : ||  ||:   :  ||:|||:||| |
    RYKDNNLIDLSGYGAKVEVYDGV--ELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYK
    430       440       450         460       470       480       490

         130       140       150       160       170       180       190
    NKIVN--VNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNYGNANGISDYINKWIFVTITN
    |  :   : |||||||||: ||||||:|   | ||||| |  |      | |     ||:|||:| ||||||
    NDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITN
    500       510        520       530       540       550       560

       200       210       220       230        240       250       260
    DRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKI-VNCSYTRYIGIRYFNIFDKELDETEIQTLYSNEPN
      |  :| |||| |     |     :     | ||       | :|  :|| ||  ||    |   |
    N-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSY
    570       580       590       600       610       620       630

      270       280       290       300       310       320            330
    TNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDSTLSINNIRSTILLANRLYSGIKVKI-------QRVN
       ||||||| |:| ||||: |    | :|  :|||       ||      :        |        : |
    SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSN
  640       650       660       670       680       690       700       710

           340       350       360       370            380       390
    NSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKTIKISSSG-----NRFNQVVVMNSVGNNCTMN
      | ||  ||| | :|  |                   ||      |      |              | :
    SQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLL
          720       730       740       750       760       770       780

    400       410       420                       430       440       X
    FKNNNGNNIGLLGFKADTVVASTWYYTHMRD----------------HTNSNGCFWNFISEEHGWQEK
    ||                   |   :   :|                     || | ||  : || |
    FKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
        790       800       810       820       830       840       850


3. US-09-910-186A-14 (1-449)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     143  Optimized Score  =     276  Significance = -1.15
Residue Identity  =     44%  Matches          =     185  Mismatches   =   192
Gaps              =      20  Conservative Substitutions              =    18

          40        50  X     60        70        80        90       100
    LISYFNKFFKRIKSSSVLNMRYKNDKYVDTSGYDSNININGDVYKYPTNKNQFGIYNDKLSEVNISQNDYII
                        ||     :| | | | |||   |   |  |||   :|   | : :     |:
                        RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                        X       10        20        30        40        50

       110       120       130       140       150       160       170
    YDNKYKNFSISFWVRIPNYDNKIVNVNNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAGINQKLAFNYGN
    |   | ||| |||:||| | | |   |||||||||| :||||||||||  ||||||||   | |:  | |
    YNSMYENFSTSFWIRIPKYFNSI-SLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQ
          60        70         80         90        100       110       120

     180       190       200       210       220       230        240
    ANGISDYINKWIFVTITNDRLGDSKLYINGNLIDQKSILNLGNIHVSDNILFKIVNCSYT-RYIGIRYFNIF
       ||||||:|||||||| ||  || |||| ||||| | |||||| | ||:||   |  | ||| |:||| |
    MINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLF
         130       140       150       160       170       180       190

    250       260       270       280       290       300               310
    DKELDETEIQTLYSNEPNTNILKDFWGNYLLYDKEYYLLNVLKPNNFIDRRKDSTLS--------INNIRST
    |||| | ||  || |  |  ||||||| || ||| ||:||   || ::|
    DKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTN
       200       210       220       230       240       250       260

          320       330       340       350       360       370       380
    ILLANRLYSGIKVKIQRVNNSSTNDNLVRKNDQVYINFVASKTHLFPLYADTATTNKEKTIKISSSGNRFNQ
    | |   || | |  | :                     |  |       |  |   |              |
    IYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ
     270       280       290       300       310       320       330
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             390       400       410           420       430       440
    VVVMNS-----VGNNCTMNFKNNNGNNIGLLGF----KADTVVASTWYYTHMRDHTNSNGCFWNFISEEHGW
    |||| |     : | | ||   |||| ||  ||         |||  ||           || | ||  : ||
    VVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGW
   340      350       360       370       380       390       400       410

      X
    QEK
     |:
    GERPL
      X
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15.res made by bobryen on Thu 7 Nov 102 14:45:08-PST.


Query sequence being compared:US-09-910-186A-15 (1-1317)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-15 (1-1317) with:
        File : US08123975A.seq

   100-
      -
N     -
U    50-
M     -
B     -
E     -
R     -
      -
O     -
F    10-
      -
S     -
E     5-
Q     -
U     -
E     -                                                              *
N     -
C     -
E     -                                                            *
S    0----------------------------------------------------------------------
      |      |      |      |      |      |      |    | | |   | | | | |
SCORE 0      63    126    189    252    315    378   441 | 504 | 567
STDEV                                               -9  -7 -5  -3 -1


                          PARAMETERS

Similarity matrix       Unitary     K-tuple                4
Mismatch penalty              1     Joining penalty       30
Gap penalty                5.00     Window size          500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                       SEARCH STATISTICS

Scores:                   Mean        Median     Standard Deviation
                          558         542          15.01

Times:                   CPU                     Total Elapsed
                    00:00:00.00                 00:00:00.00

Number of residues:                 4027
Number of sequences searched:          3
Number of scores above cutoff:         3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                         Init. Opt.
Sequence Name     Description                     Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338   567   777   0.60   0
   2. US-08-123-975A-1 Sequence 1, Application U   1338   567   777   0.60   0
               ****  1 standard deviation below mean  ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351   541   675  -1.13   0

1. US-09-910-186A-15 (1-1317)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    567  Optimized Score  =     777  Significance =  0.60
Residue Identity  =    60%  Matches          =     813  Mismatches    =   473
Gaps              =     59  Conservative Substitutions                =     0

          10    X   20        30        40        50        60        70
  GAATTCACGATGTCCTACACCAACGACAAGATCCTGATCTTGTACTTCAACAAGCTGTACAAGAAGATCAAG
                ||  | | | | | |  |   ||| | |    |||||   |      |||||| ||||
                CTCGAGCCATGGCTCG--TCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATC
                X       10          20        30        40        50

        80        90       100       110       120       130       140
  GACAACTCCATCTTGGACATGAGATACGAAAACAATAAGTTCATCGACATCTCCGGTTACGGTTCCAACATC
   | | ||||||| || || || | ||||||  |||| |  | |||||| | ||  | |||| |||||| |||
  AATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATC
    60        70        80        90       100       110       120

     150       160       170       180       190       200       210
  TCCATCAACGGTGACGTCTACATCTACTCCACCAATAGAAACCAGTTCGGAATCTACTCCTCCAAGCCTTCC
    ||||     | | ||  || || |  | | | | |  || ||| ||    | | |       |  |||||
  AACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCC
 130       140       150       160       170       180       190       200

   220       230       240       250       260       270       280
  GAGGTCAACATCGCTCAGAACAACGACATCATCTACAACGGAAGATACCAGAACTTCTCCATCTCCTTCTGG
   |  || |  |    | ||| || |  ||| | ||||||   |  ||| | |||||||||| ||||||||||
  AAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGG
         210       220       230       240       250       260       270

 290       300       310       320       330       340       350       360
  GTCCGTATCCCAAAGTACTTCAACAAGGTCAACCTGAATAACGAGTACACCATCATCGACTGCATCCGTAAC
   |||||||||| || |||||||||    ||   ||||| || || |||||||||||| |||||||    |||
  ATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAAC
       280       290       300       310       320       330       340

         370       380       390       400       410       420       430
  AATAACTCCGGATGGAAGATCTCCCTGAACTACAACAAGATCATCTGGACCCTGCAGGACACCGCCGGTAAC
  |||   || || |||||  |  || |||||||||    | ||||||||||| |||||||||||    |  | |
  AAT---TCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATC
        350       360       370       380       390       400       410

       440       450       460       470       480       490       500
  AATCAGAAGTTGGTCTTCAACTACACCCAGATGATCTCCATCTCCGACTACATCAACAAGTGGATCTTCGTC
  || |||    | || ||||| ||| | |||||||||  |||||| |||||||||||    |||||||||||
  AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
      420       430       440       450       460       470       480

     510       520       530       540       550       560       570
  ACCATCACCAATAACCGTTTGGGAAACTCCAGAATCTACATCAACGGTAACTTGATCGACGAGAAGTCCATC
  ||||||||||| || ||| ||   ||||||| |||||||||||||||     |||||||| ||||  | |||
  ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
    490       500       510       520       530       540       550

   580       590       600       610       620       630       640
  TCCAACTTGGGTGACATCCACGTCTCCGACAACATTTTGTTCAAGATCGTCGGTTGTAACGACAC---CCGT
  |||||  ||||| |||||||||  ||  | |||||  |||||||  | | |||||||   |||||   |||
  TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
   560       570       580       590       600       610       620

    650       660       670       680       690       700       710
  TACGTCGGGATCCGTTACTTCAAAGTCTTCGACACTGAGTTGGGTAAGACCGAGATCGAGACCTTGTACTCC
  ||| || |||||   ||||||||  | |||||||  ||  ||    | |  || ||| |   | |||||  |
  TACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGAC
630       640       650       660       670       680       690       700

  720       730       740       750       760       770       780
  GACGAGCCTGACCCATCCATCCTGAAGGACTTCTGGGGTAACTACCTGCTGTACAACAAACGTTACTACTTG
   || || |  |  |    |||||||| |||||||||||| ||||||||| |||| ||||||  |||||| ||
  AACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATG
        710       720       730       740       750       760       770

790       800       810       820                   830       840
  CTGAACTTGTTGCGTACCGACAAGTCCATCACCCAGAA------------CTCCAACTTCTTGAACATCAAC
  |||||  |||    | |  |||| | | |   |   ||            |  |   | | || || | ||
  CTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAA
      780       790       800       810       820       830       840

850       860       870       880       890       900       910       920
  CAGCAGAGAGGTGTCTACCAGAAGCCAAACATCTTCTCCAACACCAGATTGTACACCGGAGTCGAGGTCATT
     | | | |||        ||   | ||||||| |   ||| |     |||||   ||   | |  ||||
  GGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATC
    850       860       870       880       890       900       910

        930       940       950       960       970       980       990
  ATCAGAAAGAACGGATCTACTGATATTTCCAACACCGATAACTTCGTCAGAAAGAACGATCTGGCTTACATC
  ||||  ||  |||  |||  |         ||||  || ||  ||||  | || || ||||  |  ||||||
  ATCAAGAAATACGCGTCTGGT---------AACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATC
  920       930                940       950       960       970       980

     1000      1010      1020      1030      1040      1050      1060
  AACGTTGTCGACAGAGATGTCGAATACCGTCTGTACGCCGATATCTCTATCGCCAAACCTGAAAAGATCATC
  || ||||| |  |   |    ||||||||||||    || ||   |||   ||       ||||||||| |
  AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTG
         990      1000      1010      1020      1030      1040      1050

   1070      1080      1090      1100      1110      1120
  AAGCTGATCCGTACCTCTAACTCTAACAACTCTCTGGGACAAATCATCGTCATGGACTCC------------
         |    | | |  ||  |   ||   ||||   ||  |  | || ||| | |||
  TCTGCTCTGGAAATCCCGGACGTTGGTAA---TCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAG
      1060      1070      1080         1090      1100      1110      1120

      1130      1140      1150      1160      1170      1180      1190
  ---ATCGGTAATAACTGTACCATGAACTTCCAGAACAACAACGGTGGAAACATCGGTTTGTTGGGTTTCCAC
     |||  ||| || || |  |||||  | ||| ||||||| |||    | ||||||||  | |||||||||
  GGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCAC
       1130      1140      1150      1160      1170      1180      1190

       1200               1210      1220      1230      1240      1250
  ---TCCAAC---------AACTTGGTCGCTTCCTCCTGGTACTACAACAACATCCGTAAGAACACCTCCTCC
     | ||||         ||  |||| ||||||  ||||||| |     | |||        | |   | |
  CAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACT
     1200      1210      1220      1230      1240      1250      1260

    1260      1270      1280      1290      1300      1310      X
  AACGGTTGCTTCTGGTCCTTCATCTCCAAGGAGCACGGTTGGCAGGAGAACTAATAGGAATTC
     |||||||  |||   |||||| |    ||  ||||||||   ||         | ||  |
  CTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCT
   1270      1280      1290      1300      1310      1320      1330

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2. US-09-910-186A-15 (1-1317)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    567  Optimized Score    =    777  Significance =  0.60
Residue Identity =    60%  Matches            =    813  Mismatches   =   473
Gaps             =     59  Conservative Substitutions                =     0

          10    X   20        30        40        50        60        70
  GAATTCACGATGTCCTACACCAACGACAAGATCCTGATCTTGTACTTCAACAAGCTGTACAAGAAGATCAAG
                ||  | | | | |  |   ||| | |    |||||   |      |||||| ||||
                CTCGAGCCATGGCTCG--TCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATC
                X        10         20        30        40        50
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        80        90       100       110       120       130       140
  GACAACTCCATCTTGGACATGAGATACGAAAACAATAAGTTCATCGACATCTCCGGTTACGGTTCCAACATC
   | | ||||||| || || || | ||||||  |||| |  | |||||| | ||  | |||| |||||| |||
  AATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATC
    60        70        80        90       100       110       120

     150       160       170       180       190       200       210
  TCCATCAACGGTGACGTCTACATCTACTCCACCAATAGAAACCAGTTCGGAATCTACTCCTCCAAGCCTTCC
    ||||     | | ||  || || |  | | | | |  || ||| ||    | | |       |  |||||
  AACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCC
 130       140       150       160       170       180       190       200

   220       230       240       250       260       270       280
  GAGGTCAACATCGCTCAGAACAACGACATCATCTACAACGGAAGATACCAGAACTTCTCCATCTCCTTCTGG
   |  || |  |    | ||| || |  ||| | ||||||   |  ||| | |||||||||| ||||||||||
  AAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGG
         210       220       230       240       250       260       270

 290       300       310       320       330       340       350       360
  GTCCGTATCCCAAAGTACTTCAACAAGGTCAACCTGAATAACGAGTACACCATCATCGACTGCATCCGTAAC
   |||||||||| || |||||||||    ||   ||||| || || |||||||||||| |||||||    |||
  ATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAAC
       280       290       300       310       320       330       340

         370       380       390       400       410       420       430
  AATAACTCCGGATGGAAGATCTCCCTGAACTACAACAAGATCATCTGGACCCTGCAGGACACCGCCGGTAAC
  |||   || || |||||  | || |||||||||    | ||||||||||| |||||||||||    |  | |
  AAT---TCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATC
        350       360       370       380       390       400       410

       440       450       460       470       480       490       500
  AATCAGAAGTTGGTCTTCAACTACACCCAGATGATCTCCATCTCCGACTACATCAACAAGTGGATCTTCGTC
  || |||    | || ||||| ||| | |||||||||  |||||| |||||||||||    |||||||||||
  AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
      420       430       440       450       460       470       480

     510       520       530       540       550       560       570
  ACCATCACCAATAACCGTTTGGGAAACTCCAGAATCTACATCAACGGTAACTTGATCGACGAGAAGTCCATC
  ||||||||||| || ||| ||   ||||||| |||||||||||||||     |||||||| ||||  | |||
  ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
    490       500       510       520       530       540       550

   580       590       600       610       620       630       640
  TCCAACTTGGGTGACATCCACGTCTCCGACAACATTTTGTTCAAGATCGTCGGTTGTAACGACAC---CCGT
  |||||  ||||| |||||||||  ||  | |||||  |||||||  | | |||||||   |||||   |||
  TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
  560       570       580       590       600       610       620

    650       660       670       680       690       700       710
  TACGTCGGGATCCGTTACTTCAAAGTCTTCGACACTGAGTTGGGTAAGACCGAGATCGAGACCTTGTACTCC
  ||| || |||||   ||||||||  | |||||||  ||  ||    | |  || ||| |   | |||||  |
  TACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGAC
630       640       650       660       670       680       690       700

  720       730       740       750       760       770       780
  GACGAGCCTGACCCATCCATCCTGAAGGACTTCTGGGGTAACTACCTGCTGTACAACAAACGTTACTACTTG
   || || |  |  |    |||||||| |||||||||||| ||||||||| |||| ||||||  |||||| ||
  AACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATG
        710       720       730       740       750       760       770

790       800       810       820                   830       840
  CTGAACTTGTTGCGTACCGACAAGTCCATCACCCAGAA------------CTCCAACTTCTTGAACATCAAC
  |||||  |||    | |  |||| | | |   |   ||            |  |   | | || || | ||
  CTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAA
      780       790       800       810       820       830       840

850       860       870       880       890       900       910       920
  CAGCAGAGAGGTGTCTACCAGAAGCCAAACATCTTCTCCAACACCAGATTGTACACCGGAGTCGAGGTCATT
     | | | |||        ||   | ||||||| |   ||| |     |||||   ||   | |  ||||
  GGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATC
    850       860       870       880       890       900       910
```

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          930       940       950       960       970       980       990
    ATCAGAAAGAACGGATCTACTGATATTTCCAACACCGATAACTTCGTCAGAAAGAACGATCTGGCTTACATC
    ||||  ||  |||  |||  |         ||||  || ||  ||||  | || || ||||  |  ||||||
    ATCAAGAAATACGCGTCTGGT---------AACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATC
    920       930                940       950       960       970       980

       1000      1010      1020      1030      1040      1050      1060
    AACGTTGTCGACAGAGATGTCGAATACCGTCTGTACGCCGATATCTCTATCGCCAAACCTGAAAAGATCATC
    || ||||| |  |   |    ||||||||||||    || ||   |||   ||       ||||||||| |
    AATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTG
           990      1000      1010      1020      1030      1040      1050

     1070      1080      1090      1100      1110      1120
    AAGCTGATCCGTACCTCTAACTCTAACAACTCTCTGGGACAAATCATCGTCATGGACTCC------------
           |    | | |  ||  |   ||   ||||   ||  |  | || ||| | |||
    TCTGCTCTGGAAATCCCGGACGTTGGTAA---TCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAG
        1060      1070      1080         1090      1100      1110      1120

        1130      1140      1150      1160      1170      1180      1190
    ---ATCGGTAATAACTGTACCATGAACTTCCAGAACAACAACGGTGGAAACATCGGTTTGTTGGGTTTCCAC
       |||  ||| || || |  |||||  | ||| ||||||| |||    | ||||||||  | |||||||||
    GGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCAC
         1130      1140      1150      1160      1170      1180      1190

         1200               1210      1220      1230      1240      1250
    ---TCCAAC---------AACTTGGTCGCTTCCTCCTGGTACTACAACAACATCCGTAAGAACACCTCCTCC
       | ||||         ||  |||| ||||||  ||||||| |     | |||        | |   | |
    CAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACT
       1200      1210      1220      1230      1240      1250      1260

      1260      1270      1280      1290      1300      1310      X
    AACGGTTGCTTCTGGTCCTTCATCTCCAAGGAGCACGGTTGGCAGGAGAACTAATAGGAATTC
       |||||||  |||   |||||| |    ||  ||||||||   ||         | ||  |
    CTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCT
     1270      1280      1290      1300      1310      1320      1330

    T


3. US-09-910-186A-15 (1-1317)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =   541  Optimized Score =    675  Significance =  -1.13
Residue Identity =    54%  Matches         =    734  Mismatches   =   529
Gaps             =    90  Conservative Substitutions         =     0

   20        30        40        50        60        70        80        90
    CCAACGACAAGATCCTGATCTTGTACTTCAACAAGCTGTACAAGAAGATCAAGGACAACTCCATCTTGGACA
                         ||   ||||||||     |     | |||  | ||||   |||| || ||
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X       10        20        30        40        50

           100       110       120       130       140       150       160
    TGAGATACGAAAACAATAAGTTCATCGACATCTCCGGTTACGGTTCCAACATCTCCATCAACGGTGACGTCT
    || | ||| || |||| ||  | |||||  | || ||||||||| | ||  |     |  |||  |  ||
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90        100       110       120

         170       180       190       200       210       220       230
    ACATCTACTCCACCAATAGAAACCAGTTCGGAATCTACTCCTCCAAGCCTTCCGAGGTCAACATCGCTCAGA
    |  |       |   | |  |||||||||  | |   ||| |||      ||  || ||    |  ||||||
    AACT------GAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGA
              130       140       150       160       170       180       190

       240       250       260       270       280       290       300
    ACAACGACATCATCTACAACGGAAGATACCAGAACTTCTCCATCTCCTTCTGGGTCCGTATCCCAAAGTACT
    |  |  ||||||||| ||||     || || | |||||||  | ||||||||| |||||||||| || |||
    ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
            200       210       220       230       240       250       260

     310       320                330       340       350       360       370
    TCAACAAGGTCAACCTGAAT---------AACGAGTACACCATCATCGACTGCATCCGTAACAATAACTCCG
      ||| | |  | || ||||         || || |||||||||||| |||||||    || |||||||| |
    AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCAT---GAAGAATAACTCTG
          270       280       290       300       310          320       330

            380       390       400       410       420       430       440
    GATGGAAGATCTCCCTGAACTACAACAAGATCATCTGGACCCTGCAGGACACCGCCGGTAACAATCAGAAGT
    | |||||||||||| |   |   |||   ||||||||||| |||   || | |  |||||| |   |
    GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTG
           340       350       360       370       380       390       400

          450       460       470       480       490       500       510
    TGGTCTTCAACTACACCCAGATGATCTCCATCTCCGACTACATCAACAAGTGGATCTTCGTCACCATCACCA
    |  ||||| | |||| |           |||||| || ||||||||    ||| ||||||| ||||||||||
    TATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCA
         410       420       430       440       450       460       470

        520       530       540       550       560       570       580
    ATAACCGTTTGGGAAACTCCAGAATCTACATCAACGGTAACTTGATCGACGAGAAGTCCATCTCCAACTTGG
    ||||||   ||   ||  | | ||||||||||||||||||  ||       | |    ||||    || |
    ATAACC---TGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCC
       480          490       500       510       520       530       540

      590       600       610       620       630          640       650
    GTGACATCCACGTCTCCGACAACATTTTGTTCAAGATCGTCGGTTGTAACGA---CACCCGTTACGTCGGGA
    ||||  |   ||    ||   | ||  | |||||  | | ||||   | |||    ||||  | | || |||
    GTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
        550       560       570       580       590       600       610

       660       670       680       690       700       710       720
    TCCGTTACTTCAAAGTCTTCGACACTGAGTTGGGTAAGACCGAGATCGAGACCTTGTACTCCGACGAGCCTG
    |    ||||||    ||||| |||| ||  ||  | || || | |||||      ||||     | || ||
    TGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTT
      620       630       640       650       660       670       680

     730       740       750       760       770       780       790
    ACCCATCCATCCTGAAGGACTTCTGGGGTAACTACCTGCTGTACAACAAACGTTACTACTTGCTGAACTTGT
    || |      |||||| |||||||||||||     ||| |||||||||||   |||||  || | ||
    ACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTG
    690       700       710       720       730       740       750       760

   800       810       820       830       840       850       860
    TGCGTACCGACAAGTCCATCACCCAGAACTCCAACTTCTTGAACATCAACCAGCAGAGAGGT------GTCT
         |   ||   | |||||  | |||     |||    |       |    | ||   ||        |
    GTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACA
            770       780       790       800       810       820       830

      870       880       890       900       910       920       930
    ACCAGAAGCCAAACATCTTCTCCAACACCAGATTGTACACCGGAGTCGAGGTCATTATCAGAAAGAACGGAT
    |||||||  | ||   | ||  | ||  |    |||||| ||| |   || |||| ||| |    ||   ||
    ACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAA---AT
           840       850       860       870       880       890          900

    940       950       960       970       980       990      1000
    CTACTGATATTTCCAACACCGATAACTTCGTCAGAAAGAACGATCTGGCTTACATCAACGTTGTCGACAGAG
    |||    |   |||| ||  ||| || ||||  | ||  | ||       ||| |  || |  || ||
    CTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGA
          910       920       930       940       950       960       970

 1010      1020      1030      1040      1050      1060      1070      1080
    ATGTCGAATACCGTCTGTACGCCGATATCTCTATCGCCAAACCTGAAAAGATCATCAAGCTGATCCGTACCT
    ||   ||||  ||| | ||| || | |  |   ||   |||   ||| | |   |    |||   |  | ||
    ATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCT
          980       990      1000      1010      1020      1030      1040

         1090       1100      1110      1120             1130      1140
    CTAACTCTAAC-AACTCTCTGGGACAAATCATCGTCATGGACTC------CATCGGTAATAACTGTACCA--
    || | ||  || ||||||     || |  ||     | | |  |      || | |   ||    | |||
    CTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGC
      1050      1060      1070      1080      1090      1100      1110

       1150      1160            1170      1180      1190          1200
    TGAACTTCCAGAACAACAACG------GTGGAAACATCGGTTTGTTGGGTTTCCAC----TCCAACAACTTG
    ||   ||| ||||  |  | |       ||   | |||||| || | ||| |||||    || |  ||  ||
    TGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTG
   1120      1130      1140      1150      1160      1170      1180

    1210      1220        1230                                 1240
    GTCGCTTCCTCCTGG--TACTACAACAACATCCG---------------------------TAAGAACACCT
    ||  | |  ||   |  ||| |  || || || |                           |||   ||
    GTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAAC
 1190      1200      1210      1220      1230      1240      1250      1260

 1250               1260      1270      1280      1290      1300      1310
    CCTCCAAC---------GGTTGCTTCTGGTCCTTCATCTCCAAGGAGCACGGTTGGCAGGAGAACTAATAGG
    | | ||||         ||||||   |||   |||||| | || ||  | ||||||   ||  | |||
    CGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTC
         1270      1280      1290      1300      1310      1320      1330

        X
    AATTC
     |
    TAGAGTCGAGGCCTGCAG
       1340      1350
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-15-inv.res made by bobryen on Thu 7 Nov 102 14:45:24-PST.

Query sequence being compared:US-09-910-186A-15' (1-1317)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-15' (1-1317) with:
        File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                                            *
S    0---------------------------------------------------------------------------
      |       |      |   |  |     ||      |     ||     |   |   |      |
SCORE 0       4      9   | 13    18|     22     27     31  | 36     40
STDEV        -4         -3         -2          -1          0

                            PARAMETERS

Similarity matrix      Unitary      K-tuple                  4
Mismatch penalty             1      Joining penalty         30
Gap penalty               5.00      Window size            500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                          SEARCH STATISTICS

Scores:                    Mean         Median         Standard Deviation
                             36             29                 6.93

Times:                     CPU                         Total Elapsed
                       00:00:00.00                     00:00:00.00

Number of residues:                     4027
Number of sequences searched:              3
Number of scores above cutoff:             3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                             Init. Opt.
Sequence Name      Description                       Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U       1338    40   336   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U       1338    40   336   0.58    0
                  ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U       1351    28   200  -1.15    0


1. US-09-910-186A-15' (1-1317)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     40  Optimized Score    =     336  Significance =  0.58
Residue Identity  =    40%  Matches            =     409  Mismatches    =   518
Gaps              =     74  Conservative Substitutions                 =     0

                       X       10        20        30        40        50
                       GAATTCCTATTAGTTCTCCTGCCAACCGTGCTCCTTGGAGATGAAGGACCAG
                       ||| | |  | |  ||  |||    | |        ||| |   ||||
   TCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTG------CAGGACACTCAGGAAATC
 350       360       370       380       390             400       410

         60        70        80        90       100       110       120
   AAGCAACCGTTGGAGGAGGTGTTCTTACGGATGTTGTTGTAGTACCAGGAGGAAGCGACCAAGTTGTTGGAG
   || || |   | |        | ||  | |||| |       |   |  |         |  | | || |
   AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
          420       430       440       450       460       470       480

      130       140       150       160             170       180
   TGGAAACCCAACAAACCGATGTTTCCACCGTTGTTGTTCTGGAA------GTTCATGGTACAG----TTATT
      |   ||||||| |   ||  |    |     | | |   ||        | || |  |||      ||
   ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
      490       500       510       520       530       540       550

    190       200       210       220       230       240       250
   ACCGATGGAGTCCATGACGATGATTTGTCCCAGAGAGTTGTTAGAGTTAGAGGTACGGATCAGCTTGATGAT
    || ||   |   |   | | | ||      | |   |  | | | |    |||     | |   | |
   TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
    560       570       580       590       600       610       620

  260       270       280       290       300       310       320       330
   CTTTTCAGGTTTGGCGATAGAGATATCGGCGTACAGACGGTATTCGACATCTCTGTCGACAACGTTGATGTA
       || || |     |     || |   ||   |     |   ||| |      || |  || |  | |
   TACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGAC
  630       640       650       660       670       680       690       700

          340       350          360       370            380       390
   AGCCAGATCGTTCTTTCTGAC---GAAGTTATCGGTGTTGGAAATAT-CAGTA----GATCCGTTCTTTCTG
   | ||||  |  |  |  |  |    |||   || | | ||   |  | |||||     | |||| ||   ||
   AACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATG
          710       720       730       740       750       760       770

        400       410       420       430       440       450         460
   ATAATGACCTCGACTCCGGTGTACAATCTGGTGTTGGAGAAGATGTTTGGCTTCTGGTAGA--CACCTCTCT
    | |     |    ||||    |  |  | |   |  | ||  |   |  |  | | || |   ||||
   CTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAA
        780       790       800       810       820       830       840

        470           480       490       500       510           520
   GCTGGTTGATGTTC----AAGAAGTTGGAGTTCTGGGTGATGGACTTGTCGGTAC----GCAACAAGTTCAG
   | |    |  ||||    | ||      |  |||   |||    |||  | ||||    | | ||| ||||
   GGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGA-ACTCTTCCCTGTACCGTGGTACCAAATTCAT
      850       860       870       880        890       900       910

    530       540        550       560       570       580       590
   CAAGTAGTAACGTTTGT-TGTACAGCAGGTAGTTACCCCAGAAGTCCTTCAGGATGGATGGGTCAGGCTCGT
   ||   || ||     || ||   |  |||    || |        |  | |   || ||   |||   | ||
   CATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGT
     920       930       940       950       960       970       980

            600       610       620       630       640       650       660
   ---------CGGAGTACAAGGTCTCGATCTCGGTCTTACCCAACTCAGTGTCGAAGACTTTGAAGTAACGGA
            |  || | |  |||| | |  |  |  | | ||     |||| ||| |  |     |  | |
 AGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGAT---CTTGTCTGC
990      1000      1010      1020      1030      1040         1050

      670       680          690       700       710       720       730
 TCCCGACGTAACGGGTGTCGTTA---CAACCGACGATCTTGAACAAAATGTTGTCGGAGACGTGGATGTCAC
 ||  ||  |  |||  || | ||      |  | |   ||| |   ||          |||  || | ||||
 TCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCAC
1060      1070      1080      1090      1100      1110      1120

         740        750       760       770       780       790       800
 --CCAAGTTGGAGATGGA-CTTCTCGTCGATCAAGTTACCGTTGATGTAGATTCTGGAGTTTCCCAAACGGT
    ||| |   | ||| | || |  | | |  | | || |   ||| | | ||     | || |||   | |
 TAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAAC---GATATCGGTTTCATCGGTTTCCACCAGTT
1130    1140      1150      1160         1170      1180      1190

        810       820       830        840       850       860       870
 TATTGGTGATGGTGACGAAGATCCACTTGTTGATGTAGTCGGAGATGGAGATCATCTGGGTGTAGTTGAAGA
  |    |   | | |         ||| |||| |     | |  |      |||  | |     |||
 CAACAATATCGCTAA---------ACTGGTTGCTTCCAACTGGTACAATCGTCAGATCG--AACGTTCCTCT
1200     1210               1220      1230      1240        1250

      880       890       900       910       920       930       940
 CCAACTTCTGATTGTTACCGGCGGTGTCCTGCAGGGTCCAGATGATCTTGTTGTAGTTCAGGGAGATCTTCC
 |  |||   | ||| |   ||  || || | | || |   || | |   | || |  || |    | |
 CGCACTCTGGGTTGCTCTTGGGAGT-TCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAAC----
1260    1270      1280       1290      1300      1310      1320

    950       960       970
 ATCCGGAGTTATTGTTACGGATGCAGTCGATGA
   | |||    ||
 -CCGGGAAAGCTT
  1330      X


2. US-09-910-186A-15′ (1-1317)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    40  Optimized Score =    336  Significance =  0.58
Residue Identity =   40%  Matches         =    409  Mismatches   =   518
Gaps             =    74  Conservative Substitutions           =     0

                     X       10        20        30        40        50
                     GAATTCCTATTAGTTCTCCTGCCAACCGTGCTCCTTGGAGATGAAGGACCAG
                     ||| | |  | |  ||  |||    | |        ||| |   ||||
 TCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTG------CAGGACACTCAGGAAATC
 350       360       370       380       390             400       410

       60        70        80        90        100       110       120
 AAGCAACCGTTGGAGGAGGTGTTCTTACGGATGTTGTTGTAGTACCAGGAGGAAGCGACCAAGTTGTTGGAG
 || || |   | |        | ||  | |||| |       |   |  |         |  | | || |
 AAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
     420       430       440       450       460       470       480

    130       140       150       160             170       180
 TGGAAACCCAACAAACCGATGTTTCCACCGTTGTTGTTCTGGAA------GTTCATGGTACAG----TTATT
    |   ||||||| |   ||  |    |     | | |   ||        | || |  |||      ||
 ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
   490       500       510       520       530       540       550

  190       200       210       220       230       240       250
 ACCGATGGAGTCCATGACGATGATTTGTCCCAGAGAGTTGTTAGAGTTAGAGGTACGGATCAGCTTGATGAT
  || ||   |   |   | | | ||      | |   |  | | | |    |||     | |   | |
 TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
 560       570       580       590       600       610       620

260       270       280       290       300       310       320       330
 CTTTTCAGGTTTGGCGATAGAGATATCGGCGTACAGACGGTATTCGACATCTCTGTCGACAACGTTGATGTA
     || || |     |     || |   ||   |     |   ||| |      || |  || |  | |
 TACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGAC
630      640       650       660       670       680       690       700

        340       350          360       370            380       390
 AGCCAGATCGTTCTTTCTGAC---GAAGTTATCGGTGTTGGAAATAT-CAGTA----GATCCGTTCTTTCTG

 | ||||  |  |  |  |  |    |||   || | | ||   |  | |||||     | |||| ||   ||
 AACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATG
       710       720       730       740       750       760       770

    400       410       420       430       440       450         460
 ATAATGACCTCGACTCCGGTGTACAATCTGGTGTTGGAGAAGATGTTTGGCTTCTGGTAGA--CACCTCTCT
  | |     |    ||||    |  |  | |   |  | ||  |   |  |  | | || |   ||||
 CTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAA
     780       790       800       810       820       830       840

    470          480       490       500       510           520
 GCTGGTTGATGTTC----AAGAAGTTGGAGTTCTGGGTGATGGACTTGTCGGTAC----GCAACAAGTTCAG
 | |    |  ||||    | ||      |  |||   |||    |||  | ||||    | | ||| ||||
 GGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGA-ACTCTTCCCTGTACCGTGGTACCAAATTCAT
   850       860       870       880        890       900       910

530       540        550       560       570       580      590
 CAAGTAGTAACGTTTGT-TGTACAGCAGGTAGTTACCCCAGAAGTCCTTCAGGATGGATGGGTCAGGCTCGT
 ||   || ||     || ||   |  |||    || |        |  | |   || ||   |||   | ||
 CATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGT
  920       930       940       950       960       970       980

        600       610       620       630       640       650       660
 ---------CGGAGTACAAGGTCTCGATCTCGGTCTTACCCAACTCAGTGTCGAAGACTTTGAAGTAACGGA
          |  || | |  |||| | |  |  |  | | ||     |||| ||| |  |     |  | |
 AGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGAT---CTTGTCTGC
990      1000      1010      1020      1030      1040         1050

      670       680          690       700       710       720       730
 TCCCGACGTAACGGGTGTCGTTA---CAACCGACGATCTTGAACAAAATGTTGTCGGAGACGTGGATGTCAC
 ||  ||  |  |||  || | ||      |  | |   ||| |   ||          |||  || | ||||
 TCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCAC
1060      1070      1080      1090      1100      1110      1120

         740        750       760       770       780       790       800
 --CCAAGTTGGAGATGGA-CTTCTCGTCGATCAAGTTACCGTTGATGTAGATTCTGGAGTTTCCCAAACGGT
    ||| |   | ||| | || |  | | |  | | || |   ||| | | ||     | || |||   | |
 TAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAAC---GATATCGGTTTCATCGGTTTCCACCAGTT
1130    1140      1150      1160         1170      1180      1190

        810       820       830        840       850       860       870
 TATTGGTGATGGTGACGAAGATCCACTTGTTGATGTAGTCGGAGATGGAGATCATCTGGGTGTAGTTGAAGA
  |    |   | | |         ||| |||| |     | |  |      |||  | |     |||
 CAACAATATCGCTAA---------ACTGGTTGCTTCCAACTGGTACAATCGTCAGATCG--AACGTTCCTCT
1200     1210               1220      1230      1240        1250

      880       890       900       910       920       930       940
 CCAACTTCTGATTGTTACCGGCGGTGTCCTGCAGGGTCCAGATGATCTTGTTGTAGTTCAGGGAGATCTTCC
 |  |||   | ||| |   ||  || || | | || |   || | |   | || |  || |    | |
 CGCACTCTGGGTTGCTCTTGGGAGT-TCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAAC----
1260    1270      1280       1290      1300      1310      1320

    950       960       970
 ATCCGGAGTTATTGTTACGGATGCAGTCGATGA
   | |||    ||
 -CCGGGAAAGCTT
  1330      X


3. US-09-910-186A-15′ (1-1317)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    28  Optimized Score =    200  Significance = -1.15
Residue Identity =   43%  Matches         =    239  Mismatches   =   286
Gaps             =    28  Conservative Substitutions           =     0

       770       780 X     790       800       810       820          830
 AGTTACCGTTGATGTAGATTCTGGAGTTTCCCAAACGGTTATTGGTGATGGTGACGAAGATCCACTTG---T
                      |||  ||   ||||      |  |  ||  |||  || |||  | ||
                     ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                     X       10        20        30        40        50

        840       850         860       870       880       890
   TGATGTAGTCGGAGATGGAGATCATC--TGGGTGTAGTTGAAGACCAACTTCTGATTGTTAC--CGGCGGTG
   ||   ||     || |   |  | |||  |  || | |||   |  | |    |||    |||  ||| | ||
   TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
         60        70        80        90       100       110       120

  900            910       920       930       940       950       960
   TCCTG-----CAGGGTCCAGATGATCTTGTTGTAGTTCAGGGAGATCTTCCATCCGGAGTTATTGTTACGGA
     |||     || |  |||| | |   ||    |  ||| |  |  |||   |||||   |  |     | ||
   AACTGAATGACAAGAACCAGTTCAAACTGACCT-CTTCCGCTAACTCTAAGATCCGTGTTACT-----CAGA
      130       140       150        160       170       180            190

     970       980       990      1000      1010      1020      1030
   TGCAGTCGATGATGGTGTACTCGTTATTCAGGTTGACCTTGTTGAAGTACTTTGGGATACGGACCCAGAAGG
     |||   || ||  |  ||||  |||||    ||  ||| |     | |||  |||| || | || |||
   ATCAGAACATCATCTTCAACTCCGTATTC---CTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAAT
          200       210          220       230       240       250

  1040       1050      1060      1070      1080      1090       1100
   AGATGGA-GAAGTTCTGGTATCTTCCGTTGTAGATGATGTCGTTGTTCTGAGCGATGTTGA-CCTCGGAAGG
   | | | | || | | |      || | |     ||||   |    |  | | |    |  |   |      |
   ACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTG
 260       270       280       290       300       310       320       330

  1110      1120      1130      1140      1150      1160      1170
   CTTGGAGGAGTAGATTCCGAACTGGTTTCTATTGGTGGAGTAGATGTAGACGTCACCGTTGATGGAGATGTT
    ||||| ||      ||||   |            |||| |     | ||  ||| || | |     |    |
   GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACT-CTGATCGATATCAACGGTAAGACCAAATCT
         340       350       360       370        380       390       400

1180      1190      1200      1210      1220      1230      1240      1250
   GGAACCGTAACCGGAGATGTCGATGAACTTATTGTTTTCGTATCTCATGTCCAAGATGGAGTTGTCCTTGAT
   | |  | |        |  ||  ||||   | | | |   ||  |||    |  | |     |  || | |
   GTATTCTTCGAATACAACATCCGTGAAGACA-TCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCAC
        410       420       430        440       450       460       470

           1260      1270      1280      1290      1300      1310      X
   C---TTCTTGTACAGCTTGTTGAAGTACAAGATCAGGATCTTGTCGTTGGTGTAGGACATCGTGAATTC
   |     | || |||        |  ||||  | | | |    ||   |        ||||||    |
   CAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCG
       480       490       500       510       520       530       540 X

   TGAAGTTATCGCTAACG
     550       560
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-16.res made by bobryen on Thu 7 Nov 102 14:34:47-PST.

Query sequence being compared:US-09-910-186A-16 (1-432)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-16 (1-432) with:
        File : US08123975A.pep
    100-
       -
N      -
U    50-
M      -
B      -
E      -
R      -
       -
O      -
F    10-
       -
S      -
E     5-
Q      -
U      -
E      -
N      -
C      -
E      -                                                 * *          *
S     0----------------------------------------------------------------------
      ||     | |    | |    | |    |  |   |  |   |  |   |    |  |   |  |
SCORE 0|    23 |   46 |   69 |   92  | 116  | 139  | 162    |185   |208
STDEV -7      -6     -5     -4      -3     -2     -1        0      1

                                 PARAMETERS

Similarity matrix        PAM-150      K-tuple                    1
Threshold level of sim.      16%
Mismatch penalty               1      Joining penalty           20
Gap penalty                 5.00      Window size              432
Gap size penalty            0.05
Cutoff score                   1
Randomization group            0

                                 SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            181        165         23.64

Times:                      CPU                  Total Elapsed
                        00:00:00.00              00:00:00.00

Number of residues:                   1704
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                        Init.  Opt.
Sequence Name    Description                    Length  Score  Score   Sig.  Frame
-------------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
   1. US-08-123-975A-2 Sequence 2, Application U   850    208    264    1.14    0
                    ****  0 standard deviation from mean ****
   2. US-08-123-975A-3 Sequence 3, Application U   415    171    296   -0.42    0
   3. US-08-123-975A-5 Sequence 5, Application U   439    164    256   -0.72    0

1. US-09-910-186A-16 (1-432)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    208  Optimized Score    =    264  Significance =  1.14
Residue Identity  =    35%  Matches            =    163  Mismatches   =   231
Gaps              =     28  Conservative Substitutions                =    33

                       X       10        20        30        40        50
                       MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVY
                         |||| |||  |||    |  | || :||  |  || ||||: : :   |
   AEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVE
 380       390       400       410       420       430       440       450

         60        70        80        90       100          110       120
   IYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRNNNSG
        :|||   ||  | : : ||  ||:|  :  ||:|||:||||| |        |||||| | : ||||
   L--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSG
           460       470       480       490       500       510        520

         130       140       150       160       170       180       190
   WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLG
   ||||   |:||||| |  |      | |     ||:|||:| ||||||| | |::||||| |     |
   WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIR
          530       540       550       560        570       580       590

       200       210        220       230       240       250       260
   DIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL
   ::     | ||  |  | | ::  :|| :| |||    ||  |        ||||||| |:||| ||: |
   EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAG
        600       610       620       630       640       650       660

      270        280       290       300       310       320       330
   RTDKSITQNSNF-LNINQQRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDV
        |             |  |     : | |     |  | :  |   |  |  ||| |  |
   NKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ
      670       680       690       700       710       720       730

     340       350       360       370            380       390
   EYRLYADISIAKPEKIIKLIRTSNSNNSLGQIIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH-------
   | | |      | |    |   | |      | : :                      ||| | |
   EWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
    740       750       760       770       780       790       800

          400       410         420          X
   -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQEN
              | ||   :::       || | || |: || |
   VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
   810       820       830       840       850

2. US-09-910-186A-16 (1-432)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =    171  Optimized Score    =    296  Significance = -0.42
Residue Identity  =    49%  Matches            =    205  Mismatches   =   168
Gaps              =     17  Conservative Substitutions                =    27

   10        20        30        40        50        60        70        80
   LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVNIAQNNDII
                       ||| |  || | |:| | |   |      :||   :    | : :   | |:
                       RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                       X       10        20        30        40        50
```

```
            90       100       110       120       130       140       150
    YNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQM
    ||  | ||| |||:||||||| : |||||||| |   ||||||:||||  ||||||||    |: || | ||
    YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQM
          60        70        80         90       100       110       120

         160       170       180       190       200       210        220
    ISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFD
    | ||||||:||||||||||| ||:||||| ||| | ||||| || | ||:||  || || ||: |:||  ||
    INISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFD
        130       140       150       160       170       180       190

       230        240       250       260       270           280       290
    TELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNI
     ||   ||  ||       ||||||| || | | ||:|||    | :  |       ::    ||     ||
    KELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNI
      200       210       220       230       240       250       260

          300       310       320       330       340       350       360
    FSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS
    : |  || |   ||:| :|    | || || ||  ||||| :  ||||    | |  |||          |
    YLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNL
    270       280          290       300       310       320       330

        370           380       390           400       410       420
    LGQIIVM----DSIGNNCTMNFQNNNGGNIGLLGFHS----NNLVASSWYYNNIRKNTSSNGCFWSFISKEH
       ::        | | | || | |||  ||  |||       |||| ||   | :     || | ||  :
    SQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDD
     340       350       360       370       380       390       400

    430 X
    GWQEN
    || |
    GWGERPL
   410  X


3. US-09-910-186A-16 (1-432)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    164  Optimized Score  =    256  Significance = -0.72
Residue Identity =    35%  Matches          =    156  Mismatches   =   226
Gaps             =     28  Conservative Substitutions                =    33

            10  X     20        30        40        50        60        70
    MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVN
                |||    |  | || :||  |  || ||||: : :   |      :|||   ||  | :
                FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIR
                X       10        20        30        40          50

          80        90       100          110       120       130       140
    IAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGN
    : ||  ||:|  :  ||:|||:||||| |        |||||| | : ||||||||   |:||||| |  |
    VTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGK
    60        70        80        90       100        110       120

          150       160       170       180       190       200       210
    NQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCND-TR
         | |     ||:|||:| ||||||| | |::||||| |     |    ::     | ||  |  | |
    TKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ
  130       140       150        160       170       180       190       200

         220       230       240       250       260       270        280
    YVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNF-LNINQQR
    ::  :|| :| |||    ||  |        ||||||| |:||| ||: |       |             |
    FIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTR
           210       220       230       240       250       260       270

        290       300       310       320       330       340       350
    GVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLI
      |     : | |     |  | :  |   |  |  ||| |  |        | | |      | |    |
    SKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLA
```

```
     280       290       300       310       320       330       340

  360       370            380       390                   400       410
RTSNSNNSLGQIIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH------------SNNLVASSWYYNNIR
  | |      | : :                      ||| | |                  | ||   ::
PISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVK
   350       360       370       380       390       400       410

         420       430
KN--TSSNGCFWSFISKEHGWQEN
:       || | || |: || |
RKPYNLKLGCNWQFIPKDEGWTE
 420       430        X
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17.res made by bobryen on Thu 7 Nov 102 14:45:51-PST.


Query sequence being compared:US-09-910-186A-17 (1-1368)
Number of sequences searched:                 3
Number of scores above cutoff:                3

      Results of the initial comparison of US-09-910-186A-17 (1-1368) with:
         File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                   *
N     -
C     -
E     -                                                         *
S    0------------------------------------------------------------
      |     |     |  |  ||    | | |    |    |  | |   ||   |  ||   | |
SCORE 0    63    126 | 189|   252 |  314   |377 |  440  |503|   566
STDEV                 -9   -8  -7  -6   -5  -4   -3  -2   -1  0   1

                             PARAMETERS

Similarity matrix      Unitary   K-tuple                     4
Mismatch penalty             1   Joining penalty            30
Gap penalty               5.00   Window size               500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                          SEARCH STATISTICS

Scores:                 Mean      Median     Standard Deviation
                         520        499           39.26

Times:                  CPU                      Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:               4027
Number of sequences searched:        3
Number of scores above cutoff:       3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                        Length Score Score  Sig. Frame
-----------------------------------------------------------------------------------
                     ****  1 standard deviation above mean ****
   1. US-08-123-975A-6 Sequence 6, Application U   1351   566   797   1.17    0
                     ****  0 standard deviation from mean ****
   2. US-08-123-975A-4 Sequence 4, Application U   1338   498   706  -0.56    0
   3. US-08-123-975A-1 Sequence 1, Application U   1338   498   706  -0.56    0


1. US-09-910-186A-17 (1-1368)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    566  Optimized Score  =    797  Significance =  1.17
Residue Identity  =    61%  Matches          =    829  Mismatches   =   488
Gaps              =     39  Conservative Substitutions              =     0

          20        30        40        50        60        70        80
  TGAAGGACACCATCCTGATCCAGGTCTTCAACAACTACATCTCCAACATCTCCTCCAACGCCATCCTGTCCC
                        ||  |||||||| ||||  ||| | |||     |||   |||||||  ||
                      ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                      X       10        20        30        40        50

        90       100       110       120       130       140       150
  TGTCCTACCGTGGTGGTCGTCTGATCGACTCCTCCGGTTACGGAGCCACCATGAACGTCGGTTCCGACGTCA
  ||   |||   |       |||||||||    || |||||||| || |   |  | ||      ||  ||
  TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
        60        70        80        90       100       110       120

     160       170       180       190       200       210       220
  TCTTCAACGACATCGGTAACGGTCAGTTCAAGCTGAACAACTCCGAGAACTCCAACATCACCGCCCACCAGT
     | || |||      ||    |||||||| |||| |   ||||  ||||| || |||   |     |||
  AACTGAATGAC------AAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGA
     130             140       150       160       170       180       190

   230       240       250       260       270       280       290
  CCAAGTTCGTCGTCTACGACTCCATGTTCGACAACTTCTCCATCAACTTCTGGGTCCGTACCCCAAAGTACA
     ||  | || ||| | ||||| | |||    |||||||  |   ||||||| |||||| ||| || ||||
  ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
         200       210       220       230       240       250       260

 300       310       320       330       340       350       360       370
  ACAACAACGACATCCAGACCTACCTGCAGAACGAGTACACCATCATCTCCTGTATCAAGAACGACTCCGGTT
  | ||| |||  |||||||  ||| | || || || ||||||||||||  ||| || |||||  |||| ||||
  AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTT
       270       280       290       300       310       320       330

         380       390       400       410       420       430       440
  GGAAGGTCTCCATCAAGGGAAACCGTATCATCTGGACCCTGATCGACGTCAACGCCAAGTCCAAGTCCATCT
  ||||| ||||||||   || ||||||||||||||||| ||||||||  ||||||  ||| |||| ||  | |
  GGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTAT
     340       350       360       370       380       390       400

       450       460       470       480       490       500       510
  TCTTCGAGTACTCCATCAAGGACAACATCTCCGACTACATCAACAAGTGGTTCTCCATCACCATCACCAACG
  ||||||| |||  ||||   ||  ||||||| || ||||||||    ||||||| | | |||||||||||
  TCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATA
   410       420       430       440       450       460       470

     520       530       540       550          560       570       580
  ACCGTCTGGGTAACGCCAACATCTACATCAACGGTTCCCTGAA---GAAGTCCGAGAAGATCCTGAACCTGG
  ||   |||   || || || |||||||||||||||   ||| |    ||  |||| |  |     | ||  |
  AC---CTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTG
 480          490       500       510       520       530       540

      590       600       610       620       630       640       650
  ACCGTATCAACTCCTCCAACGACATCGACTTCAAGCTGATCAACTGTACCGACACCACCAAGTTCGTCTGGA
  |   |||   | |   |   || |||  |||||| |||  |      | |||    ||| ||||| ||||||
  AAGTTAT---CGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
  550          560       570       580       590       600       610

    660       670       680       690       700       710       720
  TCAAGGACTTCAACATCTTCGGTCGTGAGCTGAACGCCACCGAGGTCTCCTCCCTGTACTGGATCCAGTCCT
```

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   | ||  |||||  |||||||      || |||       || |  ||      | ||||  ||||||||| |
   TGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTT
    620       630       640       650       660       670       680

   730       740       750       760       770       780       790
   CCACCAACACCCTGAAGGACTTCTGGGGAAACCCACTGCGTTACGACACCCAGTACTACCTGTTCAACCAGG
    | || |   |||||| ||||||||||| || || |||   ||| |||   | |||||  |||||||    |
   ACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTG
  690       700       710       720       730       740       750       760

 800       810       820       830       840       850       860       870
   GTATGCAGAACATCTACATCAAGTACTTCTCCAAGGCCTCCATGGGTGAGACCGCCCCTCGTACCAACTTCA
   |||   |||||   ||||||||           |  |  |  | ||||| | |    ||||| |||| | ||
   GTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACA
          770       780       790       800       810       820       830

         880             890       900       910       920       930
   ACAACGCCGC------CATCAACTACCAGAACCTGTACCTGGGTCTGCGTTTCATCATCAAGAAGGCCTCCA
   || |   | |      |||||||||||   |||||||| | |||      |||||||||         || |
   ACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTA
        840       850       860       870       880       890       900

   940       950       960       970       980       990      1000
   ACTCCCGTAACATCAACAACGACAACATCGTCCGTGAGGGTGACTACATCTACCTGAACATCGACAACATCT
   ||||   | |   || ||| ||  ||||||| ||| | |  ||||||||||||||| || ||  |||| |
   ACTC---TCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCT--
         910       920       930       940       950       960       970

1010      1020      1030      1040      1050      1060      1070      1080
   CCGACGAGTCCTACCGTGTCTACGTCCTGGTCAACTCCAAGGAGATCCAGACCCAGCTGTTCCTGGCCCCAA
      |  ||   |  ||||| |||  |       ||| |||| |     |     |||| |||||||| || |
   -GAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGA
          980       990      1000      1010      1020      1030      1040

        1090      1100      1110      1120      1130      1140      1150
   TCAACGACGACCCTACCTTCTACGACGTCCTGCAGATCAAGAAGTACTACGAGAAGACCACCTACAACTGTC
   ||   ||   |       ||||| ||  | | ||||||||  | ||| ||||  || | ||||||   || |
   TCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCC
       1050      1060      1070      1080      1090      1100      1110

      1160      1170               1180      1190      1200      1210
   AGATCCTGTGCGAGAAGGA---------CACCAAGACCTTCGGACTGTTCGGTATCGGTAAGTTCGTCAAGG
   || | |||| | |||| ||          ||  |     |||| ||| ||||||||    |     || | |
   AGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATC---CACCGTTTCTACG
     1120      1130      1140      1150      1160      1170         1180

   1220      1230      1240      1250      1260      1270      1280
   ACTACGGTTACGTCTGGGACACCTACGACAACTACTTCTGTATCTCCCAGTGGTACCTGCGTCGTATCTCCG
   | |  |||  ||| |  ||    ||| |  |||||||||| |||||| | |||||||||       |
   AATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAAC
      1190      1200      1210      1220      1230      1240      1250

 1290      1300      1310      1320      1330      1340      1350      1360
   AGAACATCAACAAGCTGCGTCTGGGATGTAACTGGCAGTTCATCCCAGTCGACGAGGGTTGGACCGAGTAAT
     ||     |||| |||   ||||| || || ||||||||||||||    ||||| ||||||||||| || |
   GCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGT
    1260      1270      1280      1290      1300      1310      1320

          X
   AGGAATTC
   |     |
   AACCTCTAGAGTCGAGGCCTGCAG
  1330     X 1340      1350


2. US-09-910-186A-17 (1-1368)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    498  Optimized Score  =    706  Significance = -0.56
Residue Identity  =    54%  Matches          =    758  Mismatches   =   551
Gaps              =     70  Conservative Substitutions       =     0

        X  10        20        30        40        50        60        70
   GAATTCACGATGAAGGACACCATCCTGATCCAGGTCTTCAACAACTACATCTCCAACATCTCCTCCAACGCC
        | |||   | | | |    ||| |      |||||   | ||||||   ||||||  |   | | ||
        CTCGAGCCATGGCTC--GTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCC
        X       10          20        30        40        50        60

         80        90       100       110       120       130       140
   ATCCTGTCCCTGTCCTACCGTGGTGGTCGTCTGATCGACTCCTCCGGTTACGGAGCCACCATGAACGTCGGT
   ||||||  ||||  ||||        ||  |||||||||   ||  | ||||   |||  || ||| |||||
   ATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGT
      70        80        90       100       110       120       130

      150       160       170       180       190       200       210
   TCCGACGTCATCTTCAACGACATCGGTAACGGTCAGTTCAAGCTGAACAACTCCGAGAACTCCAACATCACC
   ||  | || | |||| |    ||||  ||   |||| || |||||  |||    ||    ||||| |||
   TCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAA
   140       150       160       170       180       190       200

    220       230       240       250       260       270       280
   GCCCACCAGTCCAAGTTCGTCGTCTACGACTCCATGTTCGACAACTTCTCCATCAACTTCTGGGTCCGTACC
   |    || |   ||     |||| ||| |||| |||| ||| |||||||||| |  ||||||| |||||| |
   GTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATC
 210       220       230       240       250       260       270       280

  290       300       310       320       330       340       350       360
   CCAAAGTACAACAACAACGACATCCAGACCTACCTGCAGAACGAGTACACCATCATCTCCTGTATCAAGAAC
   || || |||  ||||  |         | ||  ||| | || || ||||||||||||  ||| ||  | |||
   CCGAAATACTTCAACTCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAAC
         290                300       310       320       330       340

          370       380       390       400       410       420       430
   GACTCCGGTTGGAAGGTCTCCATCAAGGGAAACCGTATCATCTGGACCCTGATCGACGTCAACGCCAAGTCC
    | || |||||||| || ||  | ||          ||||||||||| |||   |||    | |  |
   AATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAA
      350       360       370       380       390       400       410

        440       450       460       470       480       490       500
   AAGTCCATCTTCTTCGAGTACTCCATCAAGGACAACATCTCCGACTACATCAACAAGTGGTTCTCCATCACC
    ||    |  | ||| | |||||    | |  ||||||||| |||||||||||    ||| ||| | | |||
   CAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACC
    420       430       440       450       460       470       480

      510       520       530       540       550       560       570
   ATCACCAACGACCGTCTGGGTAACGCCAACATCTACATCAACGGTTCCCTGAAGAAGTCCGAGAAGATCCTG
   ||||||||| | ||||||  |||| |||| ||||||||||||||    ||||   |     |   ||||
   ATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCC
  490       500       510       520       530       540       550       560

    580       590       600       610       620       630       640
   AACCTGGACCGTATCAACTCCTCCAACGACATCGACTTCAAGCTGATCAACTGTACCGACACCACCAAGTTC
   || ||||     ||| || | || ||  |||||   ||||| |||  |   |||   |||||   |   | |
   AATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTAC
          570       580       590       600       610       620       630

  650       660       670       680       690       700       710       720
   GTCTGGATCAAGGACTTCAACATCTTCGGTCGTGAGCTGAACGCCACCGAGGTCTCCTCCCTGTACTGGATC
    ||||||||||  |||||||  | ||||     || |||||||  |  ||  ||     |||||||   | |
   ATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAAC
        640       650       660       670       680       690       700

          730       740       750       760       770       780       790
   CAGTCCTCCACCAACACCCTGAAGGACTTCTGGGGAAACCCACTGCGTTACGACACCCAGTACTACCTGTTC
   ||||||    |    | |||||| |||||||||||  ||   ||||  |||||||  | ||||||| || |
   CAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTG
      710       720       730       740       750       760       770

        800       810                 820       830       840       850
   AACCAGGGTATGCAGAACATCTAC----------ATCAAGTACTTCTCCAAGGCCTCCATGGGTGAGACCGC
   || | |      | |||||  |||          |  | |||  | |||  ||  | ||||     ||  |
   AATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGG-TTACATGTACCTGAAAGG
    780       790       800       810       820        830       840

      860       870       880           890       900       910       920
   CCCTCGTACCAACTTCAACAACGCCGCCATCAAC---TACCAGAACCTGTACCTGGGTCTGCGTTTCATCAT
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     || |||       | |  |   ||  |||| ||    ||     ||||||||  |||      ||||||||
    TCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT
    850       860       870       880       890       900       910

        930       940       950       960       970       980       990
    CAAGAAGGCCTCCAACTCCCGTAACATCAACAACGACAACATCGTCCGTGAGGGTGACTACATCTACCTGAA
    ||||||    | |   ||  ||||||   ||||   |     |  |  |||  |||  |||||| |  |
    CAAGAA---ATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGT
  920          930       940       950       960       970       980

     1000      1010      1020      1030      1040      1050      1060
    CATCGACAACATCTCCGACGAGTCCTACCGTGTCTACGTCCTGGTCAACTCCAAGGAGATCCAGACCCAGCT
      |  | ||||      |  |  ||  | |  |     | ||  |||       | |||      |    ||
    AGTTAAGAACA-----AAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCT
   990           1000      1010      1020      1030      1040      1050

   1070      1080      1090      1100      1110      1120         1130
    GTTCCTGGCCCCAATCAACGACGACCCTACCTTCTACGACGTCCTGCAGATCAA---GAAGTACTACGAGAA
    | ||  |     ||||   ||||    ||   | |   | ||  |    || ||    ||| || || ||
    GCTCTGG----AAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGG
     1060          1070      1080      1090      1100      1110      1120

    1140      1150      1160      1170      1180      1190      1200
    GACCACCTACAACTGTCAGATCCTGTGCGAGAAGGACACCAAGACCTTCGGACTGTTCGGTATCGGTAAGTT
     | |||  |||| ||  | |   ||     | |||||| |||                |||| || ||
    TATCACTAACAAATGCAAAA---TGAATCTGCAGGACAACAA---------------TGGTAACGATA----
       1130      1140         1150      1160                     1170

  1210      1220      1230      1240      1250      1260      1270      1280
    CGTCAAGGACTACGGTTACGTCTGGGACACCTACGACAACTACTTCTGTATCTCCCAGTGGTACCTGCGTCG
      ||     |  ||||| |  |  |  || | |   |    |  |   |   ||| | ||||||   ||||
    --TCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCA
         1180      1190      1200      1210      1220      1230      1240

          1290      1300      1310      1320      1330      1340      1350
    TATCTCCGAGAACATCAACAAGCTGCGTCTGGGATGTAACTGGCAGTTCATCCCAGTCGACGAGGGTTGGAC
     |||     |||| |   |   |    |||||| ||    ||| |||||||||| || || || ||||||
    GATC-----GAACGT-TCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGG
            1250       1260      1270      1280      1290      1300

        1360       X
    CGAGTAATAGGAATTC
     ||      |   |
    TGAACGTCCGCTGTAACCCGGGAAAGCTT
 1310      1320    X 1330


3. US-09-910-186A-17 (1-1368)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    498  Optimized Score      =    706  Significance =  -0.56
Residue Identity =    54%  Matches              =    758  Mismatches   =    551
Gaps             =     70  Conservative Substitutions                 =      0

         X  10        20        30        40        50        60        70
    GAATTCACGATGAAGGACACCATCCTGATCCAGGTCTTCAACAACTACATCTCCAACATCTCCTCCAACGCC
         | |||   | | | |    ||| |      |||||   | ||||||   ||||||  |   | | ||
         CTCGAGCCATGGCTC--GTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCC
         X      10          20        30        40        50        60

          80        90       100       110       120       130       140
    ATCCTGTCCCTGTCCTACCGTGGTGGTCGTCTGATCGACTCCTCCGGTTACGGAGCCACCATGAACGTCGGT
    ||||||  ||||  ||||        ||  |||||||||   ||  | ||||   |||  || ||| |||||
    ATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGT
       70        80        90        100       110       120       130

       150       160       170       180       190       200       210
    TCCGACGTCATCTTCAACGACATCGGTAACGGTCAGTTCAAGCTGAACAACTCCGAGAACTCCAACATCACC
    ||  | || | |||| |    ||||  ||   |||| || |||||  |||    ||    ||||| |||
    TCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAA
    140       150       160       170       180       190       200

     220       230       240       250       260       270       280
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    GCCCACCAGTCCAAGTTCGTCGTCTACGACTCCATGTTCGACAACTTCTCCATCAACTTCTGGGTCCGTACC
    |    || |   ||     |||| ||| |||| |||| ||| |||||||||| |  ||||||| |||||| |
    GTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATC
  210       220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    CCAAAGTACAACAACAACGACATCCAGACCTACCTGCAGAACGAGTACACCATCATCTCCTGTATCAAGAAC
    || || |||  ||||  |         | ||  ||| | || || ||||||||||||  ||| ||  | |||
    CCGAAATACTTCAACTCC---------ATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAAC
          290                300       310       320       330       340

           370       380       390       400       410       420       430
    GACTCCGGTTGGAAGGTCTCCATCAAGGGAAACCGTATCATCTGGACCCTGATCGACGTCAACGCCAAGTCC
     | || |||||||| || ||  | ||          ||||||||||| |||   |||    | |  |
    AATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAA
       350       360       370       380       390       400       410

         440       450       460       470       480       490       500
    AAGTCCATCTTCTTCGAGTACTCCATCAAGGACAACATCTCCGACTACATCAACAAGTGGTTCTCCATCACC
     ||    |  | ||| | |||||    | |  ||||||||| |||||||||||    ||| ||| | | |||
    CAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACC
     420       430       440       450       460       470       480

       510       520       530       540       550       560       570
    ATCACCAACGACCGTCTGGGTAACGCCAACATCTACATCAACGGTTCCCTGAAGAAGTCCGAGAAGATCCTG
    ||||||||| | ||||||  |||| |||| ||||||||||||||    ||||   |     |   ||||
    ATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCC
   490       500       510       520       530       540       550       560

     580       590       600       610       620       630       640
    AACCTGGACCGTATCAACTCCTCCAACGACATCGACTTCAAGCTGATCAACTGTACCGACACCACCAAGTTC
    || ||||     ||| || | || ||  |||||   ||||| |||  |   |||   |||||   |   | |
    AATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTAC
           570       580       590       600       610       620       630

   650       660       670       680       690       700       710       720
    GTCTGGATCAAGGACTTCAACATCTTCGGTCGTGAGCTGAACGCCACCGAGGTCTCCTCCCTGTACTGGATC
     ||||||||||  |||||||  | ||||     || |||||||  |  ||  ||     |||||||   | |
    ATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAAC
         640       650       660       670       680       690       700

           730       740       750       760       770       780       790
    CAGTCCTCCACCAACACCCTGAAGGACTTCTGGGGAAACCCACTGCGTTACGACACCCAGTACTACCTGTTC
    ||||||    |    | |||||| |||||||||||  ||   ||||  |||||||  | ||||||| || |
    CAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTG
       710       720       730       740       750       760       770

         800       810                 820       830       840       850
    AACCAGGGTATGCAGAACATCTAC----------ATCAAGTACTTCTCCAAGGCCTCCATGGGTGAGACCGC
    || | |      | |||||  |||          |  | |||  | |||  ||  | ||||     ||  |
    AATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGG-TTACATGTACCTGAAAGG
     780       790       800       810       820       830       840

       860       870       880          890       900       910       920
    CCCTCGTACCAACTTCAACAACGCCGCCATCAAC---TACCAGAACCTGTACCTGGGTCTGCGTTTCATCAT
     || |||       | |  |   ||  |||| ||    ||     ||||||||  |||      ||||||||
    TCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCAT
    850       860       870       880       890       900       910

        930       940       950       960       970       980       990
    CAAGAAGGCCTCCAACTCCCGTAACATCAACAACGACAACATCGTCCGTGAGGGTGACTACATCTACCTGAA
    ||||||    | |   ||  ||||||   ||||   |     |  |  |||  |||  |||||| |  |
    CAAGAA---ATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGT
  920          930       940       950       960       970       980

     1000      1010      1020      1030      1040      1050      1060
    CATCGACAACATCTCCGACGAGTCCTACCGTGTCTACGTCCTGGTCAACTCCAAGGAGATCCAGACCCAGCT
      |  | ||||      |  |  ||  | |  |     | ||  |||       | |||      |    ||
    AGTTAAGAACA-----AAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCT
   990           1000      1010      1020      1030      1040      1050

   1070      1080      1090      1100      1110      1120         1130
    GTTCCTGGCCCCAATCAACGACGACCCTACCTTCTACGACGTCCTGCAGATCAA---GAAGTACTACGAGAA
   | ||  |     ||||   ||||    ||   | |   | ||  |    ||  |    ||| || || ||
   GCTCTGG----AAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGG
    1060          1070      1080      1090      1100      1110      1120

   1140      1150      1160      1170      1180      1190      1200
   GACCACCTACAACTGTCAGATCCTGTGCGAGAAGGACACCAAGACCTTCGGACTGTTCGGTATCGGTAAGTT
    | |||  |||| ||  | |   ||     | |||||| |||                |||| || ||
   TATCACTAACAAATGCAAAA---TGAATCTGCAGGACAACAA---------------TGGTAACGATA----
      1130      1140         1150      1160                     1170

 1210      1220      1230      1240      1250      1260      1270      1280
   CGTCAAGGACTACGGTTACGTCTGGGACACCTACGACAACTACTTCTGTATCTCCCAGTGGTACCTGCGTCG
     ||     |  ||||| |  |  |  || | |   |    |  |   |   ||| | ||||||   ||||
   --TCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCA
        1180      1190      1200      1210      1220      1230      1240

         1290      1300      1310      1320      1330      1340      1350
   TATCTCCGAGAACATCAACAAGCTGCGTCTGGGATGTAACTGGCAGTTCATCCCAGTCGACGAGGGTTGGAC
    |||     |||| |   |   |    |||||| ||    ||| |||||||||| || || || ||||||
   GATC-----GAACGT-TCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGG
           1250       1260      1270      1280      1290      1300

       1360       X
   CGAGTAATAGGAATTC
    ||      |   |
   TGAACGTCCGCTGTAACCCGGGAAAGCTT
1310      1320    X 1330
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> 0 <
0| |0   IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-17-inv.res made by bobryen on Thu 7 Nov 102 14:46:08-PST.


Query sequence being compared:US-09-910-186A-17'  (1-1368)
Number of sequences searched:                          3
Number of scores above cutoff:                         3

      Results of the initial comparison of US-09-910-186A-17' (1-1368) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                                          *
S    0----------------------------------------------------------------------
      ||      |     ||      |   |  |      |  |   |      ||     |      |
SCORE 0|      4     |8     12   | 16     20  |  24     28|    32     36
STDEV -4           -3          -2           -1           0

                              PARAMETERS

Similarity matrix        Unitary     K-tuple                   4
Mismatch penalty               1     Joining penalty          30
Gap penalty                 5.00     Window size             500
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                            SEARCH STATISTICS

Scores:                   Mean        Median       Standard Deviation
                           32           25              6.93

Times:                CPU                          Total Elapsed
                  00:00:00.00                      00:00:00.00

Number of residues:                     4027
Number of sequences searched:              3
Number of scores above cutoff:             3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

complement

```
                                                           Init. Opt.
Sequence Name      Description                      Length Score Score  Sig. Frame
---------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338    36   464   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U   1338    36   464   0.58    0
                  ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351    24    52  -1.15    0


1. US-09-910-186A-17' (1-1368)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score      =     36  Optimized Score   =    464  Significance =  0.58
Residue Identity   =    40%  Matches           =    563  Mismatches   =   708
Gaps               =    108  Conservative Substitutions                =     0

                        X         10        20        30        40        50
                        GAATTC--CTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGT
                        |||| |  | |  ||    || |  ||||           ||  || | | |
    GTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAAT
       20        30     X  40        50        60        70        80

             60         70        80        90       100       110
    TACATC-CCAGACGCAGCT-TGTTGATGTTCTCGGAGATACGACGCAGGTACCACTGGGAGAT----ACAGA
       ||| || ||   | || | | | |   ||   | |  | ||   ||| | |  |  |  |     | ||
    CCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
     90       100       110       120       130       140       150

     120       130       140       150       160       170       180
    AGTAGTTGTCGTAGGTGTCCCAGACGTAACCGTAGTCCTTGACGAACTTACCGATACCGAACAGTCCGAAGG
       |   |    || |    | |    | | | | || |  |  | |  |   || | ||| | | | |  |
    TCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCG
  160       170       180       190       200       210       220       230

   190       200       210       220       230       240       250       260
    TCTTGGTGTCCTTCTCGCACAGGATCTGACAGTTGTAGGTGGTCTTCTCGTAGTACTTCTTGATCTGCAGGA
    | |     ||  | |   | |   |||     |  |    | ||        | | | ||| | || ||
    TATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCT
          240       250       260       270       280       290       300

           270       280       290       300       310          320
    CGTCGTAGAAGGTAGGGTCGTCGTTGATTGGGGCCAGGAACAGCTGGGTCTGGA---TCTCCTTGGAGT---
    |   | | || | |    |     | |   |       ||||  |  |  ||||   | ||  || | |
    CTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACG
        310       320       330       340       350       360       370

     330       340       350       360       370       380       390
    TGACCAGGACGTAGACACGGTAGGACTCGTCGGAGATGTTGTCGATGTTCAGGTAGATGTAGTCACCCTCAC
         |  |  | ||| | | ||||| |   ||| ||            |||   | |||| |||    | |
    GTGAAATCATCTGGACTCTGCAGGACACTCAGGAAAT--------CAAACAGCGTGTTGTATTCAAATACTC
      380       390       400       410               420       430

   400       410       420       430        440       450       460
    GGACGATGTTGTCGTTGTTGATGTTACGGGAGTTGGAGG-CCTTCTTGATGATGAAACGCAGACCCAGGTAC
      |     |   | |   |||   |||   | | |  ||  |||| | |  || |    ||  |    | |
    TCAGATGATCAACATCTCTGA--CTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAAT
  440       450       460         470       480       490       500

  470       480       490       500       510       520       530       540
    AGGTTCTGGTAGTTGATGGCGGCGTTGTTGAAGTTGGTACGAGGGGCGGTCTCACCCATGGAGGCCTTGGAG
    |  | |      |  ||    |      |||   | |  |      || ||||     |||    | |  |
    AACTCCAAAATCTACATCAACGGCCGTCTGA---TCGACCAGAAACCGATCTCCAATCTGGGTAACATCCA-
  510       520       530       540          550       560       570

          550       560       570       580       590       600       610
    AAGTACTTGATGTAGATGTTCTGCATACCCTGGTTGAACAGGTAGTACTGGGTGTCGTAACGCAGTGGGTTT
                  | |  |    | | | || |  ||| ||       || |||||| || |     | |
    -------------CGCTTCTAATAACATCATGTTCAAACTGG-----ACGGTTGTCGTGACACTCACCGCTA
                 580       590       600            610       620       630

            620       630        640       650       660       670       680
    CCCCAG----AAGTCCTTCAGGGTGTT-GGTGGAGGACTGGATCCAGTACAGGGAGGAGACCTCGGTGGCGT
    |  | |    || | |||||   |||| |    || |||| |   |  | |      ||||||    | |
    CATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAA
          640       650       660       670       680       690       700

           690       700       710       720       730       740       750
    TCAGCTCACGACCGAAGATGTTGAAGTCCTTGATCCAGACGAACTTGGTGGTGTCGGTACAGTTGATCAGCT
     |||  ||   | |      |  ||| | |             || ||  |  |   | ||||    ||
    CCAGTCCAATTCTGGTATCCTGAAAGACTT-------------CTGGGGTGACTACCTGCAGTACGACAAAC
        710       720       730                    740       750       760

         760       770       780       790       800       810       820
    TGAAGTCGATGTCGTTGGAGGAGTTGATACGGTCCAGGTTCAGGATCTTCTCGGACTTCTTCAGGGAACCGT
     | | |  ||       |  || |   |||| |||      |     |      |    |  ||| | |||
    CGTACTACAT-------GCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGC
         770              780       790       800       810       820

       830       840       850       860       870       880             890
    TGATGTAGATGTTGGCGTTACCCAGACGGTCGTTGGTGATGGTGATGGAGAACCACTTG------TTGATGT
     |   || ||||    |  |      ||    |  || |||   |   | | | || ||      |   |||
    GG--TTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGT
      830       840       850       860       870       880       890

           900       910       920       930        940       950       960
    AGTCGGAGATGTTGTCCTTGATGGAGTACTCGAAGAAGATGGACTTGGAC-TTGGCGTTGACGTCGATCAGG
    |    |  |     | | | ||  || | |    |       ||  ||||  |  ||||  |  | || |
    ACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATC
    900       910       920       930       940       950       960

          970       980       990      1000      1010      1020      1030
    GTCCAGATGATACGGTTTCCCTTGATGGAGACCTTCCAACCGGAGTCGTTCTTGATACAGGAGATGATGGTG
    ||  | |    |  |||    | | |    ||     |  | |  | | |    || |     | | |||||
    GTGTATACATCAATGTT---GTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTG
  970       980          990      1000      1010      1020      1030

       1040      1050      1060      1070       1080      1090      1100
    TACTCGTTCTGCAGGTAGGTCTGGATGTCGTTGTTGTT-GTACTTTGGGGTACGGACCCAGAAGTTGATGGA
    ||       |   |   | ||||||  ||   |  ||| ||| | ||    | | |     ||    ||  |
    TAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCA
  1040      1050      1060      1070      1080      1090      1100      1110

      1110      1120      1130         1140      1150      1160      1170
    GAAGTTGTCGAACATGGAGTCGTAGACGA---CGAACTTGGACTGGTGGGCGGTGATGTTGGAGTTCTCGGA
      |     ||| || ||  ||    || |   | || |    |||  || |    ||| |   | | ||||
    AGA----ACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGG-
              1120      1130      1140      1150      1160      1170

       1180      1190      1200      1210      1220      1230      1240
    GTTGTTCAGCTTGAACTGACCGTTACCGATGTCGTTGAAGATGACGTCGGAACCGACGTTCATGGTGGCTCC
     ||  || | ||  ||      | | | || ||| | ||   |  |            |||    |||  |
    TTTCATCGGTTTCCAC--CAGTTCAACAATATCGCTAAACTGGTTG-----------CTTCCAACTGGTACA
   1180      1190        1200      1210      1220                 1230

     1250      1260      1270      1280       1290      1300      1310
    GTAACCGGAGGAGTCGATCAGACGACCACCACGGTAGGAC-AGGGACAGGATGGCGTTGGAGGAGATGTTGG
     |   | ||     || ||      |   |  ||| |  |  ||||    ||  || | || ||   |||||
    ATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGA-CGGTTGG
    1240      1250      1260      1270      1280      1290      1300

    1320      1330      1340      1350      1360
    AGATGTAGTTGTTGAAGACCTGGATCAGGATGGTGTCCTTCATCGTGAATT
     |     ||        ||| ||   ||  |
    GGTGAACGTCCGCTGTAACCCGGGAAAGCTT
   1310      1320      1330       X

2. US-09-910-186A-17' (1-1368)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     36  Optimized Score  =    464  Significance =  0.58
Residue Identity =    40%  Matches          =    563  Mismatches   =   708
Gaps             =    108  Conservative Substitutions             =     0

                        X         10        20        30        40        50
                        GAATTC--CTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGT
                        |||| |  | |  ||    || |  ||||           ||  || | | |
    GTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAAT
       20        30     X  40        50        60        70        80

             60         70        80        90       100       110
    TACATC-CCAGACGCAGCT-TGTTGATGTTCTCGGAGATACGACGCAGGTACCACTGGGAGAT----ACAGA
       ||| || ||   | || | | | |   ||   | |  | ||   ||| | |  |  |  |     | ||
    CCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
     90       100       110       120       130       140       150

     120       130       140       150       160       170       180
    AGTAGTTGTCGTAGGTGTCCCAGACGTAACCGTAGTCCTTGACGAACTTACCGATACCGAACAGTCCGAAGG
       |   |    || |    | |    | | | | || |  |  | |  |   || | ||| | | | |  |
    TCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCG
  160       170       180       190       200       210       220       230

   190       200       210       220       230       240       250       260
    TCTTGGTGTCCTTCTCGCACAGGATCTGACAGTTGTAGGTGGTCTTCTCGTAGTACTTCTTGATCTGCAGGA
    | |     ||  | |   | |   |||     |  |    | ||        | | | ||| | || ||
    TATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCT
          240       250       260       270       280       290       300

           270       280       290       300       310          320
    CGTCGTAGAAGGTAGGGTCGTCGTTGATTGGGGCCAGGAACAGCTGGGTCTGGA---TCTCCTTGGAGT---
    |   | | || |    |     | |   |       ||||  |  |  ||||   | ||  || | |
    CTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACG
        310       320       330       340       350       360       370

     330       340       350       360       370       380       390
    TGACCAGGACGTAGACACGGTAGGACTCGTCGGAGATGTTGTCGATGTTCAGGTAGATGTAGTCACCCTCAC
         |  |  | ||| | | ||||| |   ||| ||            |||   | |||| |||    | |
    GTGAAATCATCTGGACTCTGCAGGACACTCAGGAAAT--------CAAACAGCGTGTTGTATTCAAATACTC
      380       390       400       410               420       430

   400       410       420       430        440       450       460
    GGACGATGTTGTCGTTGTTGATGTTACGGGAGTTGGAGG-CCTTCTTGATGATGAAACGCAGACCCAGGTAC
      |     |   | |   |||   |||   | | |  ||  |||| | |  || |    ||  |    | |
    TCAGATGATCAACATCTCTGA--CTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAAT
  440       450       460         470       480       490       500

  470       480       490       500       510       520       530       540
    AGGTTCTGGTAGTTGATGGCGGCGTTGTTGAAGTTGGTACGAGGGGCGGTCTCACCCATGGAGGCCTTGGAG
    |  | |      |  ||    |      |||   | |  |      || ||||     |||    | |  |
    AACTCCAAAATCTACATCAACGGCCGTCTGA---TCGACCAGAAACCGATCTCCAATCTGGGTAACATCCA-
  510       520       530       540          550       560       570

          550       560       570       580       590       600       610
    AAGTACTTGATGTAGATGTTCTGCATACCCTGGTTGAACAGGTAGTACTGGGTGTCGTAACGCAGTGGGTTT
                  | |  |    | | | || |  ||| ||       || |||||| || |     | |
    -------------CGCTTCTAATAACATCATGTTCAAACTGG-----ACGGTTGTCGTGACACTCACCGCTA
                 580       590       600            610       620       630

            620       630        640       650       660       670       680
    CCCCAG----AAGTCCTTCAGGGTGTT-GGTGGAGGACTGGATCCAGTACAGGGAGGAGACCTCGGTGGCGT
    |  | |    || | |||||   |||| |    || |||| |   |  | |      ||||||    | |
    CATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAA
          640       650       660       670       680       690       700

           690       700       710       720       730       740       750
    TCAGCTCACGACCGAAGATGTTGAAGTCCTTGATCCAGACGAACTTGGTGGTGTCGGTACAGTTGATCAGCT
     |||  ||   | |      |  ||| | |             || ||  |  |   | ||||    ||
    CCAGTCCAATTCTGGTATCCTGAAAGACTT-------------CTGGGGTGACTACCTGCAGTACGACAAAC
        710       720       730                    740       750       760

         760       770       780       790       800       810       820
    TGAAGTCGATGTCGTTGGAGGAGTTGATACGGTCCAGGTTCAGGATCTTCTCGGACTTCTTCAGGGAACCGT
     | | |  ||       |  || |   |||| |||      |     |      |    |  ||| | |||
    CGTACTACAT-------GCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGC
         770              780       790       800       810       820

       830       840       850       860       870       880             890
    TGATGTAGATGTTGGCGTTACCCAGACGGTCGTTGGTGATGGTGATGGAGAACCACTTG------TTGATGT
     |   || ||||    |  |      ||    |  || |||   |   | | | || ||      |   |||
    GG--TTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGT
      830       840       850       860       870       880       890

           900       910       920       930       940        950       960
    AGTCGGAGATGTTGTCCTTGATGGAGTACTCGAAGAAGATGGACTTGGAC-TTGGCGTTGACGTCGATCAGG
    |    |  |     | | | ||  || | |    |       ||  ||||  |  ||||  |  | || |
    ACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATC
    900       910       920       930       940       950       960

          970       980       990      1000      1010      1020      1030
    GTCCAGATGATACGGTTTCCCTTGATGGAGACCTTCCAACCGGAGTCGTTCTTGATACAGGAGATGATGGTG
    ||  | |    |  |||    | | |    ||     |  | |  | | |    || |     | | |||||
    GTGTATACATCAATGTT---GTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTG
  970       980          990      1000      1010      1020      1030

       1040      1050      1060      1070       1080      1090      1100
    TACTCGTTCTGCAGGTAGGTCTGGATGTCGTTGTTGTT-GTACTTTGGGGTACGGACCCAGAAGTTGATGGA
    ||       |   |   | ||||||  ||   |  ||| ||| | ||    | | |     ||    ||  |
    TAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCA
  1040      1050      1060      1070      1080      1090      1100      1110

      1110      1120      1130         1140      1150      1160      1170
    GAAGTTGTCGAACATGGAGTCGTAGACGA---CGAACTTGGACTGGTGGGCGGTGATGTTGGAGTTCTCGGA
      |     ||| || ||  ||    || |   | || |    |||  || |    ||| |   | | ||||
    AGA----ACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGG-
              1120      1130      1140      1150      1160      1170

       1180      1190      1200      1210      1220      1230      1240
    GTTGTTCAGCTTGAACTGACCGTTACCGATGTCGTTGAAGATGACGTCGGAACCGACGTTCATGGTGGCTCC
     ||  || | ||  ||      | | | || ||| | ||   |  |            |||    |||  |
    TTTCATCGGTTTCCAC--CAGTTCAACAATATCGCTAAACTGGTTG-----------CTTCCAACTGGTACA
   1180      1190        1200      1210      1220                    1230

     1250      1260      1270      1280       1290      1300      1310
    GTAACCGGAGGAGTCGATCAGACGACCACCACGGTAGGAC-AGGGACAGGATGGCGTTGGAGGAGATGTTGG
     |   | ||     || ||      |   |  ||| |  |  ||||    ||  || | || ||   |||||
    ATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGA-CGGTTGG
    1240      1250      1260      1270      1280      1290      1300

    1320      1330      1340      1350      1360
    AGATGTAGTTGTTGAAGACCTGGATCAGGATGGTGTCCTTCATCGTGAATT
     |     ||        ||| ||  ||  |
    GGTGAACGTCCGCTGTAACCCGGGAAAGCTT
   1310      1320      1330       X


3. US-09-910-186A-17' (1-1368)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     24  Optimized Score  =     52  Significance = -1.15
Residue Identity =    42%  Matches          =     68  Mismatches   =    81
Gaps             =     10  Conservative Substitutions              =     0

                        X       10        20        30        40        50
                        GAATTCCTATTACTCGGTCCAACCCTCGTCGACTGGGATGAACTGCCAGTTA
                          | | | |  |||   ||    |  ||  | | ||| |      |  |||||
    GAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTC--TGCATCTCCAAATGGTACCTGAAGGAAGTTA
        1190      1200  X   1210      1220        1230      1240      1250

          60        70        80        90       100       110       120
    CATCCCAGACGCAGCTTGTTGATGTTCTCGGAGATACGACGCAGGTACCACTGGGAGATACAGAAGTAGTTG
     |  | |  || |     |  |    || ||    |    |||| |  ||    |  | ||  | || |  |
    AACGCAAACCGTACAACCTGAA---ACTGGGTTGCAATTGGCAGTT--CATCCCGAAAGACGAAGGTTG--G
        1260      1270         1280      1290        1300      1310

       130       140       150        X        170
    TCGTAGGTGTCCCAGACGTAACCGTAGTCCTTGACGAACTTACCGATACCGAACA
     |  |   ||  |      |  || || |||  |
    ACCGAATAGTAACCTCTAGAGTCG-AGGCCTGCAG
   1320      1330      1340       1350
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-18.res made by bobryen on Thu 7 Nov 102 14:35:06-PST.

Query sequence being compared:US-09-910-186A-18 (1-449)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-18 (1-449) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                              *
N     -
C     -
E     -
S    0---------------------------------------------------------------------
      |      |      |      |      |      |      |      |      |     ||
SCORE 0     23     46     69     92    115    138    161    184    207
STDEV                                                              -9

                              PARAMETERS

Similarity matrix      PAM-150    K-tuple                  1
Threshold level of sim.    16%
Mismatch penalty             1    Joining penalty         20
Gap penalty               5.00    Window size            432
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                 Mean       Median      Standard Deviation
                        206        207            0.58

Times:                  CPU                    Total Elapsed
                    00:00:00.00                00:00:00.00

Number of residues:                 1704
Number of sequences searched:          3
Number of scores above cutoff:         3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                            Init. Opt.
Sequence Name     Description                        Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                   ****  1 standard deviation above mean ****
   1. US-08-123-975A-5 Sequence 5, Application U    439   207   319   1.73   0
   2. US-08-123-975A-2 Sequence 2, Application U    850   207   326   1.73   0
                   ****  0 standard deviation from mean ****
   3. US-08-123-975A-3 Sequence 3, Application U    415   206   262   0.00   0

1. US-09-910-186A-18 (1-449)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =    207  Optimized Score   =    319  Significance =  1.73
Residue Identity =    49%  Matches           =    220  Mismatches   =   182
Gaps              =      9  Conservative Substitutions             =    33

            10        20        30        40        50        60        70
    MKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSDVIFNDIGNGQFKLNNSENSNITAHQ
             || | | |  | || | |:   ||| |||||   |   |  ||    ||||  | || |   |
             FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELND--KNQFKLTSSANSKIRVTQ
             X       10        20        30        40          50        60

          80        90       100       110       120       130       140
    SKFVVYDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSI
       ::: | |  ||: ||:| ||| |  || |  |||||| | || ||||:||:||||||||||:|:| ||:
    NQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV
           70        80        90       100       110       120       130

       150       160       170       180       190       200       210
    FFEYSIKDNISDYINKWFSITITNDRLGNANIYINGSLKKSEKILNLDRINSSNDIDFKLINCTDTTKFVWI
    |||| |:: ||:|||:|| :||||  | || ||||| |     |     : :  :| |||    | | |:|
    FFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWM
        140       150        160       170       180       190       200

     220       230       240       250       260       270       280
    KDFNIFGRELNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRTNFN
    | | ||  ||    :   | |||    ||||||||| |   ||:|| |  | |||    :  ||   |  :|
    KYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYN
       210       220       230       240       250       260       270

   290         300       310       320       330       340       350
    NAA--INYQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVLVNSKEIQTQLFLAPI
      :  |||  || | :|||:: |||  | || |||  |||||   |   |  |||     |     ||||||
    QNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-WRVYTYKYFKKEEEKLFLAPI
     280       290       300        310       320        330       340

   360         370       380       390       400       410       420
    NDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDY--GYVWDTYDNYFCISQWYLRRISEN
     |   ||   ||| | |  || || |  ||       |     : |  | | : |  ||||| |||: :
    SDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRK
     350       360       370       380       390       400       410

   430       440        X
    INKLRLGCNWQFIPVDEGWTE
       |:||||||||| ||||||
    PYNLKLGCNWQFIPKDEGWTE
   420       430        X


2. US-09-910-186A-18 (1-449)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    207  Optimized Score   =    326  Significance =  1.73
Residue Identity =    49%  Matches           =    225  Mismatches   =   186
Gaps              =      9  Conservative Substitutions             =    33

                        X       10        20        30        40        50
                        MKDTILIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSDVIFND
                          |||||  || | | |  | || | |:   ||| |||||   |   |  ||
    EKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELND
         390       400  X    410       420       430       440       450
        60        70        80        90       100       110       120
  IGNGQFKLNNSENSNITAHQSKFVVYDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTIISCIKNDSGWKVS
      ||||  | || |   |   ::: | |  ||: ||:| ||| |  || |  |||||| | || ||||:|
  --KNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKIS
       460       470       480       490       500       510       520

     130       140       150       160       170       180       190
  IKGNRIIWTLIDVNAKSKSIFFEYSIKDNISDYINKWFSITITNDRLGNANIYINGSLKKSEKILNLDRINS
  |:||||||||||:|:| ||:|||| |:: ||:|||:|| :||||  | || ||||| |     |     : :
  IRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIA
     530       540       550       560       570       580       590

   200       210       220       230       240       250       260
  SNDIDFKLINCTDTTKFVWIKDFNIFGRELNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNI
    :| |||    | | |:| | | ||  ||    :   | |||    ||||||||| |   ||:|| |  |
  NGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNS
    600       610       620       630       640       650       660

 270       280       290       300       310       320       330
  YIKYFSKASMGETAPRTNFNNAA--INYQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESY
  |||    :  ||   |  :|  :  |||  || | :|||:: |||  | || |||  |||||   |   |
  YIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSI-NDDIVRKEDYIYLDFFNLNQE-W
  670       680       690       700       710       720       730

 340       350       360       370       380       390       400
  RVYVLVNSKEIQTQLFLAPINDDPTFYDVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDY--GYVW
  |||     |     |||||| |   ||   ||| | |  || || |  ||       |     : |  | |
  RVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVF
  740       750       760       770       780       790       800

 410       420       430       440        X
  DTYDNYFCISQWYLRRISENINKLRLGCNWQFIPVDEGWTE
  : |  ||||| |||: :      |:||||||||| ||||||
  EEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
810       820       830       840       850

3. US-09-910-186A-18 (1-449)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =    206  Optimized Score  =    262  Significance =  0.00
Residue Identity  =    35%  Matches          =    151  Mismatches   =   232
Gaps              =     12  Conservative Substitutions               =    29

     10        20     X  30        40        50        60        70
  LIQVFNNYISNISSNAILSLSYRGGRLIDSSGYGATMNVGSDVIFNDIGNGQFKLNNSENSNITAHQSKFVV
                       |    ||| | |::  |:|| | |  |   |  | | | | |       :|
                      RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                      X       10        20        30        40        50

   80        90       100       110       120       130       140
  YDSMFDNFSINFWVRTPKYNNNDIQTYLQNEYTIISCIKNDSGWKVSIKGNRIIWTLIDVNAKSKSIFFEYS
  | ||::|||  ||:| ||| |      | |||||| |  | ||||||     ||||| |       : | ||
  YNSMYENFSTSFWIRIPKYFNS---ISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYS
        60        70           80        90       100       110       120

150       160       170       180       190       200       210       220
  IKDNISDYINKWFSITITNDRLGNANIYINGSLKKSEKILNLDRINSSNDIDFKLINCTDTTKFVWIKDFNI
     |||||||:|  :|||| || |: ||||| |     | ||  | :|| | |||  | || :::||| ||
  QMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNL
        130       140       150       160       170       180       190

        230       240       250       260       270       280       290
  FGRELNATEVSSLYWIQSSTNTLKDFWGNPLRYDTQYYLFNQGMQNIYIKYFSKASMGETAPRTNFNNAAIN
  | :|||  |:  ||  ||    ||||||  |  ||  ||: |    | |:     :  |    :
  FDKELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTT
      200       210       220       230       240       250       260

      300       310       320       330       340       350       360
  YQNLYLGLRFIIKKASNSRNINNDNIVREGDYIYLNIDNISDESYRVYVLVNSKEIQTQLFLAPINDDPTFY
     |   |    |         |   :            :    ||         :   |    | |
  NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLS
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  270       280       290       300       310       320       330

  370       380       390       400       410       420       430
DVLQIKKYYEKTTYNCQILCEKDTKTFGLFGIGKFVKDYGYVWDTYDNYFCISQWYLRRISENINKLRLGCN
 |   |   :    |   :   |         |  :   |:           | || | |        |||
QVVVMKSKNDQGITNKCKMNLQDNN-------GNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRT--LGCS
340       350       360              370       380       390         400

440        X
WQFIPVDEGWTE
| |||||:|| |
WEFIPVDDGWGERPL
       410 X
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19.res made by bobryen on Thu 7 Nov 102 14:46:34-PST.


Query sequence being compared:US-09-910-186A-19 (1-1242)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-19 (1-1242) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                                                         *
S    0-----------------------------------------------------------------------
      |      |      |       |     ||  |  ||  |   |  |   |   |  |   |  |
SCORE 0      12     24     37     49  |  61  |  73  |  86   | 98   |110
STDEV                            -9  -8 -7  -6  -5 -4  -3   -2 -1  0

                              PARAMETERS

Similarity matrix      Unitary     K-tuple                      4
Mismatch penalty             1     Joining penalty             30
Gap penalty               5.00     Window size                500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                           SEARCH STATISTICS

Scores:                  Mean        Median       Standard Deviation
                          106          100            6.35

Times:                   CPU                         Total Elapsed
                     00:00:00.00                      00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                             Init. Opt.
Sequence Name      Description                      Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U    1338    110   448   0.63   0
   2. US-08-123-975A-1 Sequence 1, Application U    1338    110   448   0.63   0
                   **** 1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U    1351     99   477  -1.10   0


1. US-09-910-186A-19 (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    110  Optimized Score    =    448  Significance =  0.63
Residue Identity  =    43%  Matches            =    546  Mismatches   =   580
Gaps              =    133  Conservative Substitutions               =     0

                      X       10          20        30        40       50
                      ATGGCTCTGAA--CGACCTGTGCATCAAAGTTAACAACTGGACCTGTTCTT
                      | |  ||  ||  | || |  |    ||||||   ||||  || | | ||
  CCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTT---AACTTCGATCCGATCGA
     100       110    X  120       130       140          150       160

          60        70        80        90       100       110
  CTCCCCGTCTGAAGACAACTTCACTAACGACCTGAACAAAGGCGAAGAAATCACCTCCGACACTAACAT---
  |             |    |||| |   ||      ||||  |||||  |||       |  ||| | |
  CAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATA
      170       180       190       200       210       220       230

120       130       140                150       160       170       180
  CGAAGCTGCTGAAGAAAACATCTC--------TCTGGA-CCTGATCCAGCAGTACTACCTGACTTTCAACTT
  | |  ||    | |||||| ||||        |||||| ||  |||| | | |||| |    |  ||    |
  CAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCT
    240       250       260       270       280       290       300

       190          200       210       220         230       240
  CGACAACGAA---CCGGAAAACATCTCCATCGAAAACCTGTCT--TCCGACATCATCGGTCAGCT----GGA
    |||| |||    |    | || || ||| ||||||   |||  |  || |  |||  | | ||     ||
  GAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGA
  310       320       330       340       350       360       370

    250       260       270       280       290       300
  ACTGATGCCGAACATCGAACGCTTCCCGAACGGCAAGAAATACGAACTGGACAAATA------------CAC
  | | ||   ||   |  |   |   | | |   |||  |    |   |   ||||||            ||
  AATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAA
380       390       400       410       420       430       440       450

    310       320            330       340       350        360       370
  CATGTTCCACTACCT-----GCGTGCTCAGGAATTCGAACACGGTAAATC-TCGTATCGCTCTGACTAACTC
  ||| |   ||||| |     ||  | ||     | | | |||    |||| ||  |        |  | ||
  CATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTA
        460       470       480       490       500       510       520

        380       390       400                410       420
  CGTTAACGAAGCTCTGCTGAACCCGTCTCGCGTTTAC---------ACCTTCTTCTCTTCCGACTAC-----
  | | ||||    |||| |  ||| |   |   | | |         | | ||  | ||||  |  ||
  CATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCAT
      530       540       550       560       570       580       590

                 430       440       450       460       470         480
  -----------------GTTAAGAAAGTTAACAAAGCTACTGAAGCTGCTATGTTCCTGGGTTGG--GTTGA
                   ||   || | | | |    |  ||| | |   ||  |   |  ||| |     ||
  GTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGA
    600       610       620       630       640       650       660

       490       500              510       520       530       540
  ACAGCTGGTTTACGACTTCACCGAC-------GAAACTTCTGAAGTTTCCACCACTGACAAAATCGCTGACA
  || |   |   | ||  |||  |||         |||   |  | ||       |    || |   |||
  ACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGG
  670       680       690       700       710       720       730

  550       560       570       580       590       600       610
  TCACTATCATCATCCCGTACATCGGCCCGGCTCTGAACATCGGTAACATGCTGTACAAAGACGACTTCGT--
  | |||| |  ||   ||   | | |  |  |       ||| |||  || | | ||||| |||    |||
   TGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGAT-CCGAACAAATACGTTGACGTCA
 740       750       760       770       780        790       800       810

         620       630       640               650       660       670
   ------TGGTGCTCTGATCTTCTCTGGCGCTGTTA--------TCCTGCTGGAATTCATCCCGGAAATCGCT
         | |   || |   ||   ||   |||  |        |  | |||  ||   | ||   |    |
   ACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACC
          820       830       840       850       860       870       880

     680       690       700       710       720       730       740
   ATCCCGGTTCTGGGTACCTTCGCTCTGGTTTCCTACATCGCTAACAAAGTTCTGACTGTTCAGACCATCGAC
       |  |||   ||||| | |  |    ||    ||||   || |||     | ||| | | |    | |
   TGAACTCTTCCCTGTACCGTGGTACCAAATT----CATCATCAAGAAATACGCGTCTGGTAACAAGGACAAT
        890       900       910           920       930       940       950

   750       760       770       780       790        800       810
   AACGCTCTGTCTAAACGTAACGAAAAATGGGACGAAGTTTACAAATACATCG-TTACTAACTGGCTGGCTAA
   | || ||     ||   |   | | |     | |  ||    ||  |||  |  |||   ||||||  | |
   ATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAAT
          960       970       980       990      1000      1010      1020

  820       830       840       850       860       870       880       890
   AGTTAACACTCAGATCGACCTGATCCGTAAGAAGATGAAAGAAGCTCTGGAAAACCAGGCTGAAGCTACTAA
     ||  ||  | | |  |           | |||||       |||||||||| || ||  |  | || |
   GCTTCTCAGGCTGGTGTA----------GAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCT
       1030      1040                1050      1060      1070      1080

          900       910       920       930       940       950       960
   AGCTATCATCAACTACCAGTACAACCAGTACACCGAAGAAGAAAAGAACAACATCAACTTCAACATCGATGA
     |     |||  ||   ||| |   | | ||   | ||  |    | ||  | ||| | ||| ||  ||
   GTC-----TCAGGTAGTTGTA-ATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCT
          1090      1100       1110      1120      1130      1140      1150

        970       980       990      1000      1010      1020      1030
   CCTGTCCTCTAAACTGAACGAATCCATCAACAAAGCTATGATCAACATCAACAAATTCCTGAACCAGTGCTC
    | |  |   ||    |||||   |     ||  | | |   | |  |||||||  ||   || | |
   GCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTG---GT
         1160      1170      1180      1190      1200      1210

     1040      1050      1060      1070      1080      1090      1100
   TGTTTCCTACCTGATGAACTCTATGATCCCGTACGGCGTTAAACGCCTGGAAGACTTCGACGCTTCCCTGAA
   || |||| ||  |   ||   |  |||  || |||        |  || | |  ||  |  |||     ||
   TGCTTCCAACTGGTACAATCGTCAGAT--CGAACG------TTCCTCTCGCACTCTGGGTTGCTCTTGGGAG
1220      1230      1240        1250            1260      1270      1280

   1110      1120      1130      1140      1150      1160      1170
   AGACGCTCTGCTGAAATACATCCGTGACAACTACGGTACTCTGATCGGCCAGGTTGACCGTCTGAAAGACAA
        | | | |||      |  | |  |||  | |   |      ||  || ||
   TTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
      1290      1300      1310      1320      1330       X

 1180
   GGT

2. US-09-910-186A-19 (1-1242)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score      =    110  Optimized Score    =    448  Significance =  0.63
Residue Identity   =    43%  Matches            =    546  Mismatches   =   580
Gaps               =    133  Conservative Substitutions            =     0

                       X        10          20        30        40        50
                       ATGGCTCTGAA--CGACCTGTGCATCAAAGTTAACAACTGGGACCTGTTCTT
                       | |  ||  ||  | || |  |    ||||||   ||||  || | | ||
   CCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTT---AACTTCGATCCGATCGA
      100       110    X  120       130       140          150       160

           60        70        80        90       100       110
   CTCCCCGTCTGAAGACAACTTCACTAACGACCTGAACAAAGGCGAAGAAATCACCTCCGACACTAACAT---
   |             |    |||| |   ||      ||||  |||||  |||       |  ||| | |
   CAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATA
       170       180       190       200       210       220       230
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120       130       140                150       160       170       180
  CGAAGCTGCTGAAGAAAACATCTC--------TCTGGA-CCTGATCCAGCAGTACTACCTGACTTTCAACTT
  | |  ||    | |||||| ||||        |||||| ||  |||| | | |||| |    |  ||    |
  CAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCT
    240       250       260       270       280       290       300

       190          200       210       220         230       240
  CGACAACGAA---CCGGAAAACATCTCCATCGAAAACCTGTCT--TCCGACATCATCGGTCAGCT----GGA
    |||| |||    |    | || || ||| ||||||   |||  |  || |  |||  | | ||     ||
  GAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGA
  310       320       330       340       350       360       370

    250       260       270       280       290       300
  ACTGATGCCGAACATCGAACGCTTCCCGAACGGCAAGAAATACGAACTGGACAAATA------------CAC
  | | ||   ||   |  |   |   | | |   |||  |    |   |   ||||||            ||
  AATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAA
380       390       400       410       420       430       440       450

    310       320            330       340       350        360       370
  CATGTTCCACTACCT-----GCGTGCTCAGGAATTCGAACACGGTAAATC-TCGTATCGCTCTGACTAACTC
  ||| |   ||||| |     ||  | ||     | | | |||    |||| ||  |        |  | ||
  CATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTA
        460       470       480       490       500       510       520

        380       390       400                410       420
  CGTTAACGAAGCTCTGCTGAACCCGTCTCGCGTTTAC---------ACCTTCTTCTCTTCCGACTAC-----
  | | ||||    |||| |  ||| |   |   | | |         | | ||  | ||||  |  ||
  CATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCAT
      530       540       550       560       570       580       590

                 430       440       450       460       470         480
  -----------------GTTAAGAAAGTTAACAAAGCTACTGAAGCTGCTATGTTCCTGGGTTGG--GTTGA
                   ||   || | | | |    |  ||| | |   ||  |   |  ||| |     ||
  GTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGA
    600       610       620       630       640       650       660

       490       500              510       520       530       540
  ACAGCTGGTTTACGACTTCACCGAC-------GAAACTTCTGAAGTTTCCACCACTGACAAAATCGCTGACA
  || |   |   | ||  |||  |||         |||   |  | ||       |    || |   |||
  ACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGG
  670       680       690       700       710       720       730

  550       560       570       580       590       600       610
  TCACTATCATCATCCCGTACATCGGCCCGGCTCTGAACATCGGTAACATGCTGTACAAAGACGACTTCGT--
  | |||| |  ||   ||   | | |  |  |       ||| |||  || | | ||||| |||    |||
  TGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGAT-CCGAACAAATACGTTGACGTCA
740       750       760       770       780        790       800       810

        620       630       640               650       660       670
  ------TGGTGCTCTGATCTTCTCTGGCGCTGTTA--------TCCTGCTGGAATTCATCCCGGAAATCGCT
        | |   || |   ||   ||   |||  |        |  | |||  ||   | ||   |    |
  ACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACC
         820       830       840       850       860       870       880

    680       690       700       710       720       730       740
  ATCCCGGTTCTGGGTACCTTCGCTCTGGTTTCCTACATCGCTAACAAAGTTCTGACTGTTCAGACCATCGAC
      |  |||   ||||| | |  |    ||    ||||   || |||     | ||| | | |    | |
  TGAACTCTTCCCTGTACCGTGGTACCAAATT----CATCATCAAGAAATACGCGTCTGGTAACAAGGACAAT
       890       900       910           920       930       940       950

  750       760       770       780       790        800       810
  AACGCTCTGTCTAAACGTAACGAAAAATGGGACGAAGTTTACAAATACATCG-TTACTAACTGGCTGGCTAA
  | || ||     ||   |   | | |     | |  ||    ||  |||  |  |||   ||||||  | |
  ATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAAT
         960       970       980       990      1000      1010      1020

 820       830       840       850       860       870       880       890
  AGTTAACACTCAGATCGACCTGATCCGTAAGAAGATGAAAGAAGCTCTGGAAAACCAGGCTGAAGCTACTAA
    ||  ||  | | |  |           | |||||       |||||||||| || ||  |  | || |
  GCTTCTCAGGCTGGTGTA----------GAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCT
      1030      1040                1050      1060      1070      1080
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            900       910       920       930       940       950       960
    AGCTATCATCAACTACCAGTACAACCAGTACACCGAAGAAGAAAAGAACAACATCAACTTCAACATCGATGA
      |     |||  ||   ||| |   | | ||   | ||  |    | ||  | ||| | ||| ||  ||
    GTC-----TCAGGTAGTTGTA-ATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCT
           1090      1100      1110      1120      1130      1140      1150

         970       980       990      1000      1010      1020      1030
    CCTGTCCTCTAAACTGAACGAATCCATCAACAAAGCTATGATCAACATCAACAAATTCCTGAACCAGTGCTC
     | |  |   ||    |||||   |     ||  | | |   | |  |||||||  ||   || | |
    GCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTG---GT
          1160      1170      1180      1190      1200      1210

      1040      1050      1060      1070      1080      1090      1100
    TGTTTCCTACCTGATGAACTCTATGATCCCGTACGGCGTTAAACGCCTGGAAGACTTCGACGCTTCCCTGAA
    || |||| ||  |   ||   |  |||  || |||        |  || | |  ||  |  |||     ||
    TGCTTCCAACTGGTACAATCGTCAGAT--CGAACG------TTCCTCTCGCACTCTGGGTTGCTCTTGGGAG
 1220      1230      1240        1250            1260      1270      1280

    1110      1120      1130      1140      1150      1160      1170
    AGACGCTCTGCTGAAATACATCCGTGACAACTACGGTACTCTGATCGGCCAGGTTGACCGTCTGAAAGACAA
         | | | |||      |  | |  |||  | |   |      ||  || ||
    TTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
       1290      1300      1310      1320      1330       X

  1180
    GGT

3. US-09-910-186A-19 (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     99  Optimized Score =    477  Significance = -1.10
Residue Identity =    44%  Matches         =    582  Mismatches   =   626
Gaps             =    113  Conservative Substitutions             =     0

                        X       10        20        30           40
                        ATGGCTCTGAACGACCTGTGCATCAAAGTTAACAACTGG---GACCTGTTCT
                        ||    ||||   ||||| |   |||||  |||||   |   || ||||
    ATTCCGAAATCCTGAACAATATCATCCTGA---ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTG
   20        30        40           50        60        70        80

   50        60         70        80        90        100       110       120
    TCTCCCCGTCTGAAG-ACAACTTCACTAACGACCTGAACAAAGGCGAAGAAATCACCTCCGACACTAACATC
      | |    || |||   || |  || |  |   |||||  |     |  || ||  ||  | ||| || ||
    GTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAGTTC--AAACTGACCTC
    90       100       110       120       130       140         150

           130       140       150       160       170       180       190
    GAAGCTGCTGAAGAAAACATCTCTCTGGACCTGATCCAGCAGTACTACCTGACTTTCAACTTCGACAACGAA
        | ||| |    || |||  | |    | ||  ||| |   |  | | |  | |   |||    ||
    --TTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTC
     160       170       180       190       200       210       220

         200       210       220       230       240       250       260
    CCGGAAAACATCTCCATCGAAAACCTGTCTTCCGACATCATCGGTCAGCTGGAACTGATGCCGAACATCGAA
     | |    | |||  |||   | || |   | | | | |  ||||   | | |    || |  ||     |
    TCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATAC
   230       240       250       260       270       280       290       300

       270       280       290       300       310         320       330
    CGCTTCCCGAACGGCAAGAAATACGAACTGGACAAATACACCATGTTCCAC--TACCTGCGTGCTCAGGAAT
      | ||   ||| ||| |||  |  |    |      | | |    ||| |  || | |  |  || ||| |
    ACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACT
           310       320       330       340       350       360       370

       340                    350        360       370       380       390
    TCGAAC-------ACGGT------AAATCTCGTATC-GCTCTGACTAACTCCGTTAACGAAGCTCTGCTGAA
      || |       |||||      ||||||    ||  |    || |  ||||| ||   | ||   |||||
    CTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGTGAAGACATCT---CTGAA
         380       390       400       410       420       430          440

         400       410       420       430       440       450       460
    CCCGTCTCGCGTTTACACCTTCTTCTCTTCCGACTACGTTAAGAAAGTTAACAAAGCTACTGAAGCTGCTAT
      | ||   ||    |   ||||||  | ||  |  |   || ||  | ||||| ||||   ||  || |
    TACATCAATCG----CTGGTTCTTCGTTACCATCACC---AATAACCTGAACAATGCTA--AAATCTACATC
          450           460       470          480       490         500

       470       480         490       500       510       520       530
    GTTCCTGGGTTGGGTTGAACAGCTG--GTTTACGACTTCACCGACGAAACTTCTGAAGTTTCCACCACTGAC
         |    |||  |  |   | |   |  | ||| ||   || |  |   || | | |   | ||    |
    AACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTC
       510       520       530       540       550       560       570

          540       550                560       570       580       590
    AAAAT---CGCTGACATCACT---------ATCATCATCCCGTACATCGGCCCGGCTCTGAACATCGGTAAC
    ||| |   || |||||||  |          |||||     | |   |  | |     | |||| ||
    AAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTG
     580       590       600       610       620       630       640

       600       610       620       630       640       650       660
    ATGCTGTACAAAGACGACTTCGTTGGTGCTCTGATCTTCTCTGGCGCTGTTATCCTGCTGGAATTC------
       | || |||   |||    |   |      ||||   |||  | | |    ||||   || |||
    TCTCAGTCCAATATCGA---AGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGT
   650       660          670       680       690       700       710

           670       680       690       700       710       720
    ATCCCGGAAATCGCTATCCCGGTTCTGGGTACCTTCGCTCTGGTTTCCTACATCGCTAACAAAGTTCT----
    |  |||   ||    | |   |       ||  |||  |   | |  | | | | || |||     ||
    AATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAG
    720       730       740       750       760       770       780

      730       740         750       760       770       780       790
    ---GACTGTTCAGACCATCGA--CAACGCTCTGTCTAAACGTAACGAAAAATGGGACGAAGTTTACAAATAC
       |||| | | |    |  |  |    |||  || |||   ||| | || |   |  |  |  || |   |
    AAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGC
  790       800       810       820       830       840       850       860

        800       810       820       830       840       850       860
    ATC--GTTACTAACTGGCTGGCTAAAGTTAACACTCAGATCGACCTGATCCGTAAGAAGATGAAAGAAGCTC
      |  ||   |   ||    | | |   |    | || ||| | ||  || ||      ||||    | |
    GACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACT-CTCAGTCCATCAATGATGACATCGT
          870       880       890       900        910       920       930

      870       880       890       900                            910
    TGGAAAACCAGGCTGAAGCTACTAAAGCTATCATCAAC---------------------TACCAGTACAACC
      | |||  || ||  | ||||     || || |||||                     |||   |||||
    ACGTAAAGAAGACTACATCTACCTGGACT-TCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGT
          940       950       960        970       980       990      1000

     920       930       940       950       960       970       980
    AGTACACCGAAGAAGAAAAGAACAACATCAACTTCAACATCGATGACCTGTCCTCTAAACTGAACGAATCCA
    | | ||   |||||||| | ||     ||         |||  |||    |||    ||||  || |  |||
    ACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGA---TTCCGACGAACTCTACAACACCA
         1010      1020      1030      1040        1050      1060      1070

   990          1000      1010      1020      1030      1040      1050
    TC---AACAAAG-CTATGATCAACATCAACAAATTCCTGAACCAGTGCTCTGTTTCCTACCTGATGAACTCT
    ||   | |||||  || ||  |||| |         ||   |   |||| |       |  ||| ||| |||
    TCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAA-TCT
         1080      1090      1100      1110      1120      1130      1140

    1060      1070      1080      1090      1100      1110      1120
    ATGATCCCGTACGGCGTTAAACGCCTGGAAGACTTCGACGCTTCCCTGAAAGACGCTCTGCTGAAATACATC
    |    |     ||  | |    |  |  |    ||| |||  ||    |  |      |  |  || |   |
    ACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCG------TATTCGAAGAATAC
        1150      1160      1170      1180      1190            1200

  1130       1140      1150      1160      1170      1180         1190
    CGTGACAACTACGGTACTCTGATCGGCCAGGTTGACCGTCTGAAAGACAAGGTTAACAAC---ACCCTGTCT
       ||| ||| | | |     |   |  |  |  |     | |||  |||     |||||   |  |||  |
    AAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGT
 1210       1220      1230      1240      1250      1260      1270      1280

   1200      1210      1220      1230      1240 X
    ACTGACATCCCGTTCCAGCTGTCCAAATACGTTGACAACCAGTAA
        |    | ||||   | |    |  | | |   | | | ||
TGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCC
     1290      1300      1310      1320      1330      1340
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-19-inv.res made by bobryen on Thu 7 Nov 102 14:46:49-PST.

Query sequence being compared:US-09-910-186A-19' (1-1242)
Number of sequences searched:                        3
Number of scores above cutoff:                       3

      Results of the initial comparison of US-09-910-186A-19' (1-1242) with:
        File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                                *
N     -
C     -
E     -                                *
S    0-----------------------------------------------------------------------
      |      |      |      |    | |      |       | |    |      |      ||
SCORE 0      8      17     25   |34      42     51 |   59     68      76
STDEV       -2                  -1                 0                  1

                         PARAMETERS

Similarity matrix      Unitary     K-tuple                  4
Mismatch penalty             1     Joining penalty         30
Gap penalty               5.00     Window size            500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                         SEARCH STATISTICS

Scores:                  Mean       Median     Standard Deviation
                           63           39        21.94

Times:                   CPU                   Total Elapsed
                   00:00:00.00                 00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name     Description                      Length Score Score  Sig. Frame
---------------------------------------------------------------------------------
  1. US-08-123-975A-4 Sequence 4, Application U    1338    76   209   0.59    0
  2. US-08-123-975A-1 Sequence 1, Application U    1338    76   209   0.59    0
               **** 1 standard deviation below mean ****
  3. US-08-123-975A-6 Sequence 6, Application U    1351    38   442  -1.14    0

1. US-09-910-186A-19' (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     76  Optimized Score    =     209  Significance =  0.59
Residue Identity  =    39%  Matches            =     246  Mismatches   =   332
Gaps              =     48  Conservative Substitutions               =     0

   640       650       660       670       680       690       700       710
    TGTACAGCATGTTACCGATGTTCAGAGCCGGGCCGATGTACGGGATGATGATAGTGATGTCAGCGATTTTGT
                         ||    |  |||   | | | |  |      | |||   || | |     |
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

           720       730       740       750       760       770
    CAGTGGTGGAAACTTCAGAAGTTTCGTCGGTGAAGTCGTAAACCAGCTGTTCAACCCAACCCAGGA------
    ||    |   | || ||       | |  |  | |     || || ||| || |||   | |   |
    CATCAAT---ACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTC
             60        70        80        90       100       110       120

     780       790       800       810         820       830       840
    ACATAGCAGCTTCAGTAGCTTTGTTAACTTTCTTAACGTAGTC--GGAAGAGAAGAAGGTGTAAACGCGAGA
      | | || | || ||      ||||||||   |    | | |  | |  |||   || |||  |  |  ||
    CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGA
          130       140       150       160       170       180       190

     850       860           870                   880       890       900
    CGGGTTCAGCAGAG----CTTCGTTAACGGAGTTA------------GTCAGAGCGATACGAGATTTACCGT
        | ||  |  |      || | ||    | ||             |  |  ||| |     |  |||
    ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTC
        200       210       220       230       240       250       260

         910       920       930       940       950       960
    GTTCGAATTCCTGAGCACGCAGGTAGTGGAACATGGTGTATTTGTCCAGTTCGTATTTCTT-----GCCGTT
     |||    |||  | | || |  || |  |||    | | | ||  || |   ||   | |      | |
    CTTCTGGATCCGTATCCCG-AAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCA
      270       280       290       300       310       320       330

  970       980       990      1000        1010      1020      1030
    CGGGAAGCGTTCGATGTTCGGCATCAGTTCCAGCTGAC--CGATGATGTCGGAAGACAGGTTTTCGATGGAG
     || || |  |    ||| |  |  |  ||      ||   ||     || | |  | |     |  |   |
    TGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGG
     340       350       360       370       380       390       400

 1040      1050                 1060      1070      1080      1090      1100
    ATGTTTTCCGGTTCGTTG-----------TCGAAGTTGAAAGTCAGGTAGTACTGCTGGATCAGGTCCAGAG
    |  |    | |   ||||           ||  || |||    ||  |   ||| |   |  |   |  ||
    AAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCA--ATCGCTGGAT
   410       420       430       440       450       460         470

          1110      1120      1130      1140      1150      1160      1170
    AGATGTTTTCTTCAGCAGCTTCGATGTTAGTGTCGGAGGTGATTTCTTCGCCTTTGTTCAGGTCGTTAGTGA
        |||  | ||| || |     | | | |  |         | | ||  |     || | |||      |
    CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAA
   480       490       500       510       520       530       540       550

        1180      1190      1200      1210      1220      1230      1240 X
    AGTTGTCTTCAGACGGGGAGAAGAACAGGTCCCAGTTGTTAACTTTGATGCACAGGTCGTTCAGAGCCAT
    |    ||| ||  | |||  |    || |   |   |   | | |      || || || |    |  |
    ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACAC
           560       570       580       590       600       610       620

    TCACCGCTACATCTGGAT
         630       640
```

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2. US-09-910-186A-19' (1-1242)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    76  Optimized Score    =    209  Significance =  0.59
Residue Identity =   39%  Matches            =    246  Mismatches   =   332
Gaps             =    48  Conservative Substitutions                =     0

  640       650       660       670       680       690       700       710
   TGTACAGCATGTTACCGATGTTCAGAGCCGGGCCGATGTACGGGATGATGATAGTGATGTCAGCGATTTTGT
                        ||    |  |||   | | | |  |      | |||   || | |     |
                       CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                       X        10       20        30        40        50

          720       730       740       750       760       770
   CAGTGGTGGAAACTTCAGAAGTTTCGTCGGTGAAGTCGTAAACCAGCTGTTCAACCCAACCCAGGA------
   ||    |   | || ||       | |  |  | |     || || ||| || |||   | |   |
   CATCAAT---ACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTC
            60        70        80        90       100       110       120

    780       790       800      810         820       830       840
   ACATAGCAGCTTCAGTAGCTTTGTTAACTTTCTTAACGTAGTC--GGAAGAGAAGAAGGTGTAAACGCGAGA
     | | || | || ||      ||||||||   |    | | |  | |  |||   || |||  |  |  ||
   CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGA
         130       140       150       160       170       180       190

    850       860           870                   880       890       900
   CGGGTTCAGCAGAG----CTTCGTTAACGGAGTTA------------GTCAGAGCGATACGAGATTTACCGT
       | ||  |  |      || | ||    | ||             |  |  ||| |     |  |||
   ATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTC
       200       210       220       230       240       250       260

        910       920       930       940       950       960
   GTTCGAATTCCTGAGCACGCAGGTAGTGGAACATGGTGTATTTGTCCAGTTCGTATTTCTT-----GCCGTT
    |||    |||  | | || |  || |  |||    | | | ||  || |   ||   | |      | |
   CTTCTGGATCCGTATCCCG-AAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCA
     270       280        290       300       310       320       330

 970       980       990      1000        1010      1020      1030
   CGGGAAGCGTTCGATGTTCGGCATCAGTTCCAGCTGAC--CGATGATGTCGGAAGACAGGTTTTCGATGGAG
    || || |  |    ||| |  |  |  ||      ||   ||     || | |  | |     |  |   |
   TGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGG
    340       350       360       370       380       390       400

1040      1050                 1060      1070      1080      1090      1100
   ATGTTTTCCGGTTCGTTG-----------TCGAAGTTGAAAGTCAGGTAGTACTGCTGGATCAGGTCCAGAG
   |  |    | |   ||||           ||  || |||    ||  |   ||| |   |  |   |  ||
   AAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCA--ATCGCTGGAT
  410       420       430       440       450       460         470

         1110      1120      1130      1140      1150      1160      1170
   AGATGTTTTCTTCAGCAGCTTCGATGTTAGTGTCGGAGGTGATTTCTTCGCCTTTGTTCAGGTCGTTAGTGA
       |||  | ||| || |     | | | |  |         | | ||  |     || | |||      |
   CTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAA
  480       490       500       510       520       530       540       550

       1180      1190      1200      1210      1220      1230      1240 X
   AGTTGTCTTCAGACGGGGAGAAGAACAGGTCCCAGTTGTTAACTTTGATGCACAGGTCGTTCAGAGCCAT
   |    ||| || | ||| |    || |   |   |   | | |      || || || |    |  |
   ACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACAC
          560       570       580       590       600       610       620

   TCACCGCTACATCTGGAT
        630       640

3. US-09-910-186A-19' (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =    38  Optimized Score    =    442  Significance = -1.14
Residue Identity =   40%  Matches            =    524  Mismatches   =   681
Gaps             =    79  Conservative Substitutions                =     0
```

```
           10   X    20        30        40        50        60        70
   TTACTGGTTGTCAACGTATTTGGACAGCTGGAACGGGATGTCAGTAGACAGGGTGTTGTTAACCTTGTCTTT
                | |  |||  |||  |  ||           |  |||   |  |  | | | ||  ||
                ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTA
                X       10        20        30        40        50

          80        90       100       110       120       130          140
   CAGA-CGGTCAACCTGGCCGATCAGAGTACCGTAGTTGTCACGGATGTATTTCAGCAGAGCGT---CTTTCA
   || |     ||| |||  ||||| |  |      | ||  |  | || | |  |  |  | ||     |  |
   CAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAA
  60        70        80        90       100       110       120       130

          150       160       170       180       190       200       210
   GGGAAGCGTCGAAGTCTTCCAGGCGTTTAACGCCGTACGGGATCATAGAGTTCATCAGGTAGGAAACAGAGC
    |  |    | |  ||   | | | | |  |||        |     | |||  ||||      ||||
   TGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCAT
         140       150       160       170       180       190       200

        220       230       240       250       260       270       280
   ACTGGTTCAGGAATTTGTTGATGTTGATCATAGCTTTGTTGATGGATTCGTTCAGTTTAGAGGACAGGTCAT
     |       | |||  | ||  |   |  |  |||        |  ||    | |  |      | |  ||
   CTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTAT
       210       220       230       240       250       260       270

      290       300       310       320       330       340       350
   CGATGTTGAAGTTGATGTTGTTCTTTTCTTCTTCGGTGTACTGGTTGTACTGGTAGTTGATGATAGCTTTAG
   | |   | |  |  |   ||       | || ||     ||||  || |        | |   | | | |
   CCAGAATTACATCCACAATGAATACACCATCATC----AACTGCATGAA-----GAATAACTCTGGTTGGAA
     280       290       300           310       320            330

    360       370       380       390         400       410        420
   TAGCTTCAGCCTGGTTTTCCAGAGCTTCTTTCATCT--TCTTACGGATCAGGTCGATCTGA-GTGTTAACTT
    | || || ||  | |  ||  | | |||    |||  ||      | | |   || |  |  |||   |||
   GATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTT
  340       350       360       370       380       390       400       410

     430       440       450       460          470       480       490
   TAGCCAGCCAGTTAGTAACGATGTATTTGTAAACTTC---GTCCCATTTTTCGTTACGTTTAGACAGAGCGT
        |     | ||  | ||  | | || | || ||     |   || ||||||||  | |   | | | |
   CGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCT
          420       430       440       450       460       470       480

      500                510          520       530       540       550
   TGTCGATGGT---------CTGAACAGT---CAGAACTTTGTTAGCGATGTAGGAAACCAGAGCGAAGGTAC
      | ||| |          | ||| ||   | | | | |  || |||  |   | ||    | ||||  ||
   GAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTAT
        490       500       510       520       530       540       550

      560       570          580          590       600       610       620
   CCAGAACCGGGATAGCGATTTC---CGGGA---TGAATTCCAGCAGGATAACAGCGCCAGAGAAGATCAGAG
   |   ||| | || | |   |||   | |||   |||  || | |      |   |  | |     |  |
   CGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTT
      560       570       580       590       600       610       620

                  630       640       650       660       670       680
   CACCA--------ACGAAGTCGTCTTTGTACAGCATGTTACCGATGTTCAGAGCCGGGCCGATGTACGGGAT
   | |||        ||  |   ||||  || ||  ||   |     || ||    |  | |    | ||
   CTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATA
    630       640       650       660       670       680       690

      690       700       710       720       730       740         750
   GATGATAGTGATGTCAGCGATTTGTCAGTGGTGGAAACTTCAGAAGTTTCGTCGGTGAA--GTCGTAA-AC
     ||| ||   | |  |  | |    |  || || | |    ||||   |    | | ||   | |||| |
   CCTGAAAGACTTCTGGGGTAAT---CCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAA
  700       710       720          730       740       750       760

       760       770       780       790       800         810       820
   CAGCTGTTCAACCCAACCCAGGAACATAGCAGCTTCAGTAGCTTTGTTAACT--TTCTTAACGTAGTCGGAA
    | || ||  | | |||  | |||     |  |    |  |   |  | |||  |||  ||   |  | |||
   GAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAA
   770       780       790       800       810       820       830

        830       840       850       860       870       880       890
   -GAGAAGAAGGTGTAAACGCGAGACGGGTTCAGCAGAGCTTCGTTAACGGAGTTAGTCAGAGCGATACGAGA
       ||  |  |  |    || |||  || || | | |    ||| |     | |  |   || |  | |
   CTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCA-----TCATCCGTCGCAAATCTAAC
 840       850       860       870       880            890       900

      900       910       920       930       940       950       960
   TTTACCGTGTTCGAATTCCTGAGCACGCAGGTAGTGGAACATGGTGTATTTGTCCAGTTCGTATTTCTTGCC
   | |       ||  | |  |||   || | |||    || | |      |   || |  | | ||
   TCTCAGTCCATC--AATGATGACATCGTACGTA----AAGAAGACTACATCTACCTGGACTTCTTCAACCTG
    910         920       930           940       950       960       970

    970       980       990      1000      1010               1020
   GTTCGGGAAGCGTTCGATGTTCGGCATCAGTTCCAGCTGACCGATGA---------TGTCGGAAGACAGGTT
     || ||||  |   |         |  ||| |     ||  || ||         | ||      | | |
   AATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAAAGCTTTTCCTGGCTCCGATC
        980       990      1000      1010      1020      1030      1040

1030      1040      1050      1060      1070      1080      1090      1100
   TTCGATGGAGATGTTTTCCGGTTCGTTGTCGAAGTTGAAAGTCAGGTAGTACTGCTGGATCAGGTCCAGAGA
   |  |||   || |   ||     |    || |  |  ||    | |  | || ||  || |   ||  |  |
   TCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGC-CGACCTACTCTTGCCA
     1050      1060      1070      1080      1090       1100      1110

         1110      1120      1130      1140      1150      1160
   GATG-TTTTCTTCAGCAGCTTCGATGTTAGTGTCGGAGGTGATTTCTTCGCCTTTGTTCAGGT---CGTTAG
   | || | |||   |        ||   || || || |   | | |  |||   |    |   |   ||
   GCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATC
    1120      1130      1140      1150      1160      1170      1180

1170      1180      1190      1200      1210      1220      1230      1240
   TGAAGTTGTCTTCAGACGGGGAGAAGAACAGGTCCCAGTTGTTAACTTTGATGCACAGGTCGTTCAGAGCCA
   ||   | || |||  |       ||||  |  ||    |  . || |   |     |||  ||| |  || |
   TGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAA
  1190      1200      1210      1220      1230      1240      1250

   X
   T

   ACCGTACAACCTGAAACTGGG
1260      1270      1280
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-20.res made by bobryen on Thu 7 Nov 102 14:35:30-PST.


Query sequence being compared:US-09-910-186A-20 (1-413)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-20 (1-413) with:
         File : US08123975A.pep

      100-
         -
N        -
U     50-
M        -
B        -
E        -
R        -
         -
O        -
F     10-
         -
S        -
E      5-
Q        -
U        -
E        -
N        -
C        -
E        -  **                                                     *
S      0-----------------------------------------------------------------
          |     |     |     |     |     |     |     |     |     |
SCORE 0     29    58    87    116   144   173   202   231   260
STDEV         0                             1


                         PARAMETERS

Similarity matrix       PAM-150    K-tuple                     1
Threshold level of sim.     16%
Mismatch penalty              1    Joining penalty            20
Gap penalty                5.00    Window size               413
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                       SEARCH STATISTICS

Scores:                   Mean       Median       Standard Deviation
                           97          17           140.59

Times:                   CPU                      Total Elapsed
                     00:00:00.00                  00:00:00.00

Number of residues:                    1704
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                      Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                   ****  1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U    850    260    297   1.16   0
                   ****  0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U    415     17    181  -0.57   0
  3. US-08-123-975A-5 Sequence 5, Application U    439     16    179  -0.58   0


1. US-09-910-186A-20 (1-413)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    260  Optimized Score  =    297  Significance =  1.16
Residue Identity  =    45%  Matches          =    189  Mismatches   =   198
Gaps              =      5  Conservative Substitutions            =    19

      X     10        20        30        40        50        60        70
    MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIEN
          || | | ||||      |  || | | |   |     |            |    |
      APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINE-----LILDTDLISKIELPSE
      X       10        20        30        40             50        60

          80        90       100       110       120       130       140
    LSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFSSDYV
                |  |: |  ||   |  | | || :| |      |:|| |  :|||   :|| ||| ||:
    NTESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYI
       70        80        90       100       110       120       130

       150       160       170       180       190       200       210
    KKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVI
    |  ||  ||::| ||| | | ||  |     | ||||||  |:|||| |||:||   |  |  |   :|| |
    KTANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
    140       150       160       170       180       190       200

     220       230       240       250       260       270       280
    LLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEA
    |||||||  ||| | | | ||| ||   : |||||| |||||| : |  ||  ||: ||||   |:  |  |
    LLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
  210       220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    LENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSMIPYGVKR
    |  || |   || | || | | || |||    |  ||||| || |  ||| | | |||||||  ||| :| :
    LNYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
         290       300       310       320       330       340       350

          370       380       390       400       410   X
    LEDFDASLKDALLKYIRDNYGTLIGQVDRLKDKVNNTLSTDIPFQLSKYVDNQ
    | |||  ||  || || :|   |||  :  | |||  | |  || || |
    LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIIL
       360       370       380       390       400      X 410       420

    N


2. US-09-910-186A-20 (1-413)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     17  Optimized Score  =    181  Significance = -0.57
Residue Identity  =     9%  Matches          =     41  Mismatches   =   342
Gaps              =      5  Conservative Substitutions            =    25

        X       10        20        30        40        50        60
        MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENI
          | ||               |             |          |        : |      |
    RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
        X   10        20        30        40        50        60        70

    70        80        90       100       110       120       130       140
    SIENLSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEALLNPSRVYTFFS
```

```
        |  :      :  |      | |  |        |        :        :| :      ::
    NSISLNNEYTIINCMENN-----SGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTIT
          80        90            100       110       120       130

           150       160       170       180       190       200       210
    SDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFS
                : :                      |   |    |      |    :  |:        |
    NNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQS
  140       150       160       170       180       190       200       210

         220       230       240       250       260       270       280
    GAVILLEFIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQIDLIRKK
     : || :|  :        : |  |  ||   |  :                       :        | ||
    NSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKK
          220       230       240       250       260       270       280

       290       300       310       320       330       340       350
    MKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSMIPY
       :           :         | :   |         |         |        |
    YASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCK
        290       300       310       320       330       340       350

     360       370       380       390       400       410  X
    GVKRLEDFDASLKDALLKYIRDNYGTLIGQVDRLKDKVNNTLSTDIPFQLSKYVDNQ
                  :   :             |  ::   ||     |
    MNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
      360       370       380       390       400       410 X


3. US-09-910-186A-20 (1-413)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     16  Optimized Score   =    179  Significance = -0.58
Residue Identity =    11%  Matches           =     47  Mismatches   =   340
Gaps             =     20  Conservative Substitutions              =    18

            10        20        30        40        50        60        70
    MALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIEN
                          |     |   :           : : |    |: ||             |
            FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQN
            X        10        20        30        40        50        60

          80        90       100       110       120           130       140
    LSSDIIGQLELMPNIERFPNGKKYELDKYTMFHYLRAQEFEHGKSRIALTNSVNEAL----LNPSRVYTFFS
         :          | |  |      |    |                            |      ||
    IIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFE
        70        80        90       100       110       120       130

           150       160       170       180       190       200       210
    SDYVKKVNKATEAAMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKDDFVGALIFS
          :        |      |                |  ||  :|              :  |:    ||
    YNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFS
     140       150       160       170       180       190       200

                220       230       240       250       260       270
    GAVILLE-------FIPEIAIPVLGTFALVSYIANKVLTVQTIDNALSKRNEKWDEVYKYIVTNWLAKVNTQ
         |        :        |  |       ||        |  |    | |     | |      |
    IFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSK
   210       220       230       240       250       260       270       280

    280                290       300       310       320       330       340
    IDLIRK---------KMKEALENQAEATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKF
        |          : |       :       | |  :         :                      |
    YINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEF
           290       300       310       320       330       340       350

           350       360       370       380       390       400       410
    LNQCSVSYLMNSMIPYGVKRLEDFDASLKDALLKYIRDNYGTLIGQVDRLKDKVNNTLSTDIPFQLSKYVDN
     |   :                  : |  :  |  |   |   |   :
    YNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKL
         360       370       380       390       400       410       420

    X
```

```
Q

GCNWQFIPKDEGWTE
X  430
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-21.res made by bobryen on Thu 7 Nov 102 14:47:13-PST.


Query sequence being compared:US-09-910-186A-21 (1-1242)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

      Results of the initial comparison of US-09-910-186A-21 (1-1242) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                              *
N     -
C     -
E     -                                                               *
S    0----------------------------------------------------------------------
      |      ||     |    |  |      |      |  |   |    | |      | |    |
SCORE 0     13|    27    | 40    53     67   | 80     |93    107 |  120
STDEV        -4        -3        -2        -1         0          1

                              PARAMETERS

Similarity matrix      Unitary    K-tuple                    4
Mismatch penalty             1    Joining penalty           30
Gap penalty               5.00    Window size              500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                   Mean        Median      Standard Deviation
                            98          89          18.48

Times:                     CPU                    Total Elapsed
                       00:00:00.00                00:00:00.00

Number of residues:                   4027
Number of sequences searched:            3
Number of scores above cutoff:           3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                       Length Score Score  Sig. Frame
-----------------------------------------------------------------------------------
                   ****  1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U  1351   120   320   1.19    0
                   ****  0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U  1338    88   394  -0.54    0
  3. US-08-123-975A-1 Sequence 1, Application U  1338    88   394  -0.54    0


1. US-09-910-186A-21 (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    120  Optimized Score  =    320  Significance =  1.19
Residue Identity =     40%  Matches          =    359  Mismatches   =   486
Gaps              =     46  Conservative Substitutions              =     0

                        X       10                20        30        40
                        ATGGCTCCAGGAATCTG--------TATCGACGTCGACAACGAGGACTTGTT
                            | |||  || |||        ||    |  |  |||||   |  ||
    CAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGA
     450       460       470       480       490       500       510

        50        60        70        80        90          100       110
    CTTCATCGCTGACAAGAACTCCTTCTCCGACGACTTGTCCAAGAACGAGAGAA---TCGAGTACAACACCCA
     |  |   | ||||  ||   | ||   || |   |  | ||    || |  |   || |     ||    |
    ATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGA
   520       530       540       550       560       570       580       590

        120       130       140       150       160       170          180
    GTCCAACTACATCGAGAACGACTTCCCAATCAACGAGTTGATCTTGGACACCGACTTG---ATCTCCAAGAT
       | |    | | ||  |  ||     |   ||   |  |||||  |||||||  ||      ||||| ||
    CATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATAT
           600       610       620       630       640       650       660

         190                200       210       220       230       240
    CGAGTTGCCATCCGAGA---------ACACCGAGTCCTTGACTGACTTCAACGTCGACGTCCCAGTCTACGA
    |||    |  | | |||         || |||| | | |||  ||||||   |   |    |   | ||| |
    CGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAA
         670       680       690       700       710       720       730

      250       260       270       280       290       300       310
    GAAGCAACCAGCTATCAAGAAGATTTTCACCGACGAGAACACCATCTTCCAATACCTGTACTCTCAGACCTT
     ||  ||     |||    ||   |   | | |  |      ||||   |   |     |||||| |
    CAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGG
       740       750       760       770       780       790       800

    320       330          340       350       360       370       380
    CCCTTTGGACATCAGAGACA---TCTCCTTGACCTCTTCCTTCGACGACGCCCTGCTGTTCTCCAACAAGGT
         |    |   |   ||    |  |  || ||||   | |  | ||  ||      | | || |   |
    TGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGA
     810       820       830       840       850       860       870

     390       400       410       420       430       440       450
    CTACTCCTTCTTCTCCATGGACTACATCAAGACTGCTAACAAGGTCGTCGAGGCCGGTTTGTTCGCTGGTTG
      | | | || ||       | |  | |       | | ||| |  | |   |   ||      |
    AAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACAT
   880       890       900       910       920       930       940       950

   460       470         480       490        500       510       520
    GGTCAAGCAGATCGTCAAC--GATTTCGTCATCGAGGCTA-ACAAGTCCAACACCATGGACAAGATTGCCGA
       |  | |  || |||||  || |  |  || | |  || |||  | |||   | |  | ||    |  ||
    CTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGA
           960       970       980       990      1000      1010      1020

    530       540       550       560       570       580       590
    CATCTCCTTGATTGTCCCATACATCGGTTTGGCCTTGAACGTCGGTAACGAGACCGCCAAGGGTAACTTCGA
     |     ||  | |  ||   |   | ||  | |     |  |   | |        ||| |   ||  |||
    AAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGA
        1030      1040      1050      1060      1070      1080      1090

  600                610       620       630       640       650         660
    GAA-------CGCTTTCGAGATCGCTGGTGCCTCCATCTTGTTGGAGTTCATCCCAGAGTTG--TTGATCCC
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      |         || | |  | |    || |    |   ||  | |  |  |  |  | | |   |||||
    ACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGG
      1100      1110      1120      1130      1140      1150      1160

         670       680       690       700       710       720       730
    AGTCGTCGGTGCCTTCTTGTTGGAGTCCTACATCGACAACAAGAACAAGATCATCAAGACCATCGACAACGC
      ||  | ||  || |   |  |    |    ||||  |  | ||  |   | ||   | |  | |
    TATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTA
    1170      1180      1190      1200      1210      1220      1230

       740       750       760       770       780       790       800
    TTTGACCAAGAGAAACGAGAAGTGGTCCGACATGTACGGTTTGATCGTCGCCCAATGGTTGTCCACCGTCAA
      |||   |    ||    ||   || | || || |        | |    | | |||  || || |   ||
    CCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAA------ACTGGGTTGCAATTGGCAGTTCATCCCGAA
  1240      1250      1260      1270            1280      1290      1300

     810       820       830         840          X      860       870
    CACCCAATTCTACACCATCAAGGAGGGTATGTA--CAAGGCCTTGAACTACCAGGCCCAAGCTTTGG
       | ||   |  |||    || |   | |  |  | ||||||  |
    AGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCCTGCAG
      1310      1320      1330      1340      1350

2. US-09-910-186A-21 (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     88  Optimized Score  =    394  Significance = -0.54
Residue Identity =    41%  Matches          =    459  Mismatches   =   582
Gaps             =     77  Conservative Substitutions              =     0

      140       150     X 160       170       180       190       200
    TTCCCAATCAACGAGTTGATCTTGGACACCGACTTGATCTCCAAGATCGAGTTGCCATCCGAGAACACCGAG
                        || |  |   | || |   ||     || |  | |   | ||  ||| | ||
                        CTCGAGCCATGGCTCG---TCTGCTGTCTACCTTC--ACTGAATACATCAAG
                        X       10           20        30          40

    210       220       230       240       250       260       270
    TCCTTGACTGACTTCAACGTCGACGTCCCAGTCTACGAGAAGCAACCAGCTATCAAGAAGATTTTCACCGAC
      | | |   |   |  | ||     ||    ||||||     | |     ||| |   |  |  |  ||
    AACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCT
     50        60        70        80        90       100       110

  280       290        300       310       320       330       340
    GAGAACACCATCTTCCAAT-ACCTGTACTCTCAGACCTTCCCTTTGGACATCAGAGACATCTCCT-----TG
       || | || | ||   |     ||   ||  || |    |       ||||||  || ||  |     ||
    TCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTG
  120       130       140       150       160       170       180       190

      350       360       370       380       390       400       410
    ACCTCTTCCTTCGACGACGCCCTGCTGTTCTCCAACAAGGTCTACTCCTTCTTCTCCATGGACTACATCAAG
       ||||||     ||| |   | |||      || || |    |   | |  ||| ||| ||
    GAATCTTCCAAAATCGAAGTTATCCTG------AAGAATGCTATCGTATACAACTCTATGTAC---------
          200       210               220       230       240

    420       430       440       450       460       470       480
    ACTGCTAACAAGGTCGTCGAGGCCGGTTTGTTCGCTGGTTGGGTCAAGCAGATCGTCAACGATTTCGTCATC
           | ||  ||  |    ||   | | ||  |     |    |    | |  || |  | |   ||
    ------GAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAAT
         250       260       270       280       290       300       310

  490       500       510       520             530       540       550
    GAGGCTAACAAGTCCAACACCATGGACAAGATTGCCG------ACATCTCCTTGATTGTCCCATACATCGGT
    ||    | ||    ||||  |||||| || | | | |      |  | ||  |||    |    | |||
    GAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATC
       320       330       340       350       360       370       380

      560       570       580       590       600       610       620
    TTGGCCTTGAACGTCGGTAACGAGACCGCCAAGGGTAACTTCGAGAACGCTTTCGAGATCGCTGGTGCCTCC
    | | |  || | | |  | | || | |    || ||    |    ||    |   ||||         |  |
    TGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGAT------GATCAAC
     390       400       410       420       430       440            450

    630       640       650       660       670       680       690
    ATCTTGTTGGAGTTCATCCCAGAGTTGTTGATCCCAGTCGTCGGTGCCTTCTTGTTGGAGTCCTACATCGAC
    ||||      |  |||  |    | | ||  |  |  ||  |          ||    | ||| | ||| ||
    ATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTAC
         460       470       480       490       500       510       520

  700           710       720       730       740       750
    AACAAGAAC---AAGATCATCAAGACCATCGACAACGCTTTGACCAAGAGAAACG---------AGAAGTGG
    | |||   |     ||||  | |||       |  |  | ||   || |   |||         | |    |
    ATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATG
       530       540       550       560       570       580       590

  760       770       780       790       800        810       820       830
    TCCGACATGTACGGTTTGATCGTCGCCCAATGGTTGTCCACCGTC-AACACCCAATTCTACACCATCAAGGA
    | | |  || ||||||     | | | ||  | |    |    || || ||   | |||   | |  ||| |
    TTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAA
     600       610       620       630       640       650       660

           840       850            860       870       880       890
    GGGTATGTACAAGGCCTTGAA-----CTACCAGGCCCAAGCTTTGGAGGAGATCATCAAGTACAGATACAAC
      | | | | |||   |  ||      ||| |   |||  |       |  ||| | ||  ||   |
    CTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGT
   670       680       690       700       710       720       730       740

    900       910       920       930       940       950       960
    ATCTACTCCGAGAAGGAGAAGTCCAACATTAACATCGACTTCAACGACATCAACTCCAAGCTGAACGAGGGT
      ||||    || | || ||  |  ||   |   |  |  |  ||||    |||    |  |  |||
    GACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACG-----
           750       760       770       780       790       800

  970       980       990      1000      1010      1020      1030      1040
    ATTAACCAGGCCATCGACAACATCAACAACTTCATCAACGGTTGTTCCGTCTCCTACTTGATGAAGAAGATG
     | ||| | |       |  |    |||  | | | || |||      |  ||     |||  |  || ||
    -TCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACAT-
     810       820       830       840       850       860       870

         1050      1060      1070      1080      1090      1100      1110
    ATTCCATTGGCCGTCGAGAAGTTGTTGGACTTCGACAACACCCTGAAGAAGAACTTGTTGAACTACATCGAC
     | ||      | ||        || | ||  | |   || | | |||||  ||  ||      |||  |||
    CTACCTGAACTCTTCCCTGTACCGTGGTAC--CAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGAC
    880       890       900         910       920       930       940

       1120       1130      1140      1150      1160      1170      1180
    GAGAACAAGTTGTAC-TTGATCGGTTCCGCTGAGTACGAGAAGTCCAAGGTCAACAAGTACTTGAAGACCAT
     | | |       ||  ||||||  |   |         | |||  |||  |||  | |||     | | |
    AATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGT-TAAGAACAAAGAATACCGTCTGGCTAC
    950       960       970       980       990      1000      1010

      1190      1200      1210      1220      1230      1240 X
    CATGCCATTCGACTTGTCCATCTACACCAACGACACCATCTTGATCGAGATGTTCTAA
    ||    || |  ||    |   |  |  || ||     |||     |  |    |  |
    CA----ATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGT
  1020          1030      1040      1050      1060      1070 X    1080

    CTCAGG
    1090

3. US-09-910-186A-21 (1-1242)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     88  Optimized Score  =    394  Significance = -0.54
Residue Identity =    41%  Matches          =    459  Mismatches   =   582
Gaps             =     77  Conservative Substitutions              =     0

      140       150     X 160       170       180       190       200
    TTCCCAATCAACGAGTTGATCTTGGACACCGACTTGATCTCCAAGATCGAGTTGCCATCCGAGAACACCGAG
                        || |  |   | || |   ||     || |  | |   | ||  ||| | ||
                        CTCGAGCCATGGCTCG---TCTGCTGTCTACCTTC--ACTGAATACATCAAG
                        X       10           20        30          40

    210       220       230       240       250       260       270
    TCCTTGACTGACTTCAACGTCGACGTCCCAGTCTACGAGAAGCAACCAGCTATCAAGAAGATTTTCACCGAC
      | | |   |   |  | ||     ||    ||||||     | |     ||| |   |  |  |  ||
  AACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCT
   50        60        70        80        90       100       110

280       290       300       310       320       330       340
  GAGAACACCATCTTCCAAT-ACCTGTACTCTCAGACCTTCCCTTTGGACATCAGAGACATCTCCT-----TG
     || | || | ||   |     ||   ||  || |    |       ||||||  || ||  |     ||
  TCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTG
120       130       140       150       160       170       180       190

    350       360       370       380       390       400       410
  ACCTCTTCCTTCGACGACGCCCTGCTGTTCTCCAACAAGGTCTACTCCTTCTTCTCCATGGACTACATCAAG
     ||||||     ||| |   | |||      || || |    |   | |  ||| ||| ||
  GAATCTTCCAAAATCGAAGTTATCCTG------AAGAATGCTATCGTATACAACTCTATGTAC---------
      200       210                 220       230       240

  420       430       440       450       460       470       480
  ACTGCTAACAAGGTCGTCGAGGCCGGTTTGTTCGCTGGTTGGGTCAAGCAGATCGTCAACGATTTCGTCATC
         | ||  ||  |    ||   | | ||  |     |    |     | |  || |  | |   ||
  ------GAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAAT
      250       260       270       280       290       300       310

490       500       510       520                 530       540       550
  GAGGCTAACAAGTCCAACACCATGGACAAGATTGCCG------ACATCTCCTTGATTGTCCCATACATCGGT
  ||    | ||    ||||  |||||| || | | | |      |  | ||  |||    |    | |||
  GAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATC
    320       330       340       350       360       370       380

   560       570       580       590       600       610       620
  TTGGCCTTGAACGTCGGTAACGAGACCGCCAAGGGTAACTTCGAGAACGCTTTCGAGATCGCTGGTGCCTCC
  | | |  || | | |  | | || | |    || ||    |    ||    |   ||||         |  |
  TGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGAT------GATCAAC
  390       400       410       420       430       440                450

  630       640       650       660       670       680       690
  ATCTTGTTGGAGTTCATCCCAGAGTTGTTGATCCCAGTCGTCGGTGCCTTCTTGTTGGAGTCCTACATCGAC
  ||||      |  |||  |    | | ||  |  |  ||   |          ||    |  ||| | ||| ||
  ATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTAC
      460       470       480       490       500       510       520

700           710       720       730       740       750
  AACAAGAAC---AAGATCATCAAGACCATCGACAACGCTTTGACCAAGAGAAACG---------AGAAGTGG
  | |||   |     ||||  | |||       |  |  | ||   || |   |||         |  |   |
  ATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATG
    530       540       550       560       570       580       590

760       770       780       790       800       810       820       830
  TCCGACATGTACGGTTTGATCGTCGCCCAATGGTTGTCCACCGTC-AACACCCAATTCTACACCATCAAGGA
  | | |  || ||||||     | | | ||  | |    |    || || ||   | |||   | |  ||| |
  TTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAA
   600       610       620       630       640       650       660

          840       850                 860       870       880       890
  GGGTATGTACAAGGCCTTGAA-----CTACCAGGCCCAAGCTTTGGAGGAGATCATCAAGTACAGATACAAC
    | | | | |||   |  ||      ||| |   |||  |       |   ||| | ||  ||   |
  CTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGT
670       680       690       700       710       720       730       740

  900       910       920       930       940       950       960
  ATCTACTCCGAGAAGGAGAAGTCCAACATTAACATCGACTTCAACGACATCAACTCCAAGCTGAACGAGGGT
    ||||    || | || ||  |  ||   |   |  |  |  ||||    |||    |  |  |||
  GACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACG-----
            750       760       770       780       790       800

970       980       990      1000      1010      1020      1030      1040
  ATTAACCAGGCCATCGACAACATCAACAACTTCATCAACGGTTGTTCCGTCTCCTACTTGATGAAGAAGATG
   | ||| | |       |  |    |||  | | | || |||      |  ||     |||  |  || ||
  -TCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACAT-
   810       820       830       840       850       860       870

        1050      1060      1070      1080      1090      1100      1110
  ATTCCATTGGCCGTCGAGAAGTTGTTGGACTTCGACAACACCCTGAAGAAGAACTTGTTGAACTACATCGAC
   | ||      | ||         || | ||  | |   || | | |||||  ||  ||      |||  |||
  CTACCTGAACTCTTCCCTGTACCGTGGTAC--CAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGAC
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  880       890       900       910       920       930       940

    1120      1130      1140      1150      1160      1170      1180
  GAGAACAAGTTGTAC-TTGATCGGTTCCGCTGAGTACGAGAAGTCCAAGGTCAACAAGTACTTGAAGACCAT
   | | |       ||  ||||||  |   |         | |||  |||  |||  | |||     | | |
  AATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGT-TAAGAACAAAGAATACCGTCTGGCTAC
  950       960       970       980       990      1000      1010

   1190      1200      1210      1220      1230      1240 X
  CATGCCATTCGACTTGTCCATCTACACCAACGACACCATCTTGATCGAGATGTTCTAA
  ||    || |  ||    |   |  |  || ||     |||     |  |    |  |
  CA----ATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGT
1020            1030      1040      1050      1060      1070 X    1080

  CTCAGG
  1090
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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-21-inv.res made by bobryen on Thu 7 Nov 102 14:47:31-PST.

Query sequence being compared:US-09-910-186A-21' (1-1242)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

     Results of the initial comparison of US-09-910-186A-21' (1-1242) with:
       File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                             *
N     -
C     -
E     -                                                           *
S    0---------------------------------------------------------------------
      |      |      |      |      |      |     ||  |   ||   | ||  | |
SCORE 0      7     14     22     29     36     43  |  51|   |58|  |65
STDEV                                         -9  -7   -5  -3 -2  0

                                PARAMETERS

Similarity matrix        Unitary      K-tuple                        4
Mismatch penalty               1      Joining penalty               30
Gap penalty                 5.00      Window size                  500
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                              SEARCH STATISTICS

Scores:                 Mean        Median        Standard Deviation
                          63            62              2.31

Times:                  CPU                       Total Elapsed
                    00:00:00.00                   00:00:00.00

Number of residues:                   4027
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
    1. US-08-123-975A-4 Sequence 4, Application U   1338    65   457   0.87    0
    2. US-08-123-975A-1 Sequence 1, Application U   1338    65   457   0.87    0
    3. US-08-123-975A-6 Sequence 6, Application U   1351    61   448  -0.87    0

1. US-09-910-186A-21' (1-1242)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     65  Optimized Score   =    457  Significance =  0.87
Residue Identity  =    42%  Matches           =    556  Mismatches   =   657
Gaps              =    108  Conservative Substitutions               =     0

                       X        10        20        30        40
                       TTAGAACATCTCGATCAAGATGGTGTCGTTGGTGTAGATG---GACAAGTCG
                        || | ||     ||||  |     ||  |  || |  ||    || | ||
   CTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCC
     20        30        40        50        60        70        80

  50        60           70        80        90      100            110
   AATGGCATGATGG---TCTTCAAGTACTTGTTGACCTTGGACTTCTCGTACTCAG------CGGAACCGATC
   |||  | |||| |   | |     |||   |  |   |  || ||   |    ||        || ||||||
   AATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATC
  90       100       110      120       130       140       150       160

        120       130       140                     150       160
   AAGTACAACTTGTTCTCGTCGATGTAGTTCAA-------------CAAGTTCTTCTTCAGGGTGTTGTCG--
    |  | ||   | ||  |  | |  |  |  |              ||||| | ||  ||  || | |||
   GACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTA
         170       180       190       200       210       220       230

           170      180       190       200                      210
   ---------AAGTCCAACAACTTCTCGACGGCCAATGGAAT---------------CATCTTCTTCATCAAG
            | || | | |||||||| ||  ||    | ||                  |  || ||||
   TACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
       240       250       260       270       280       290       300

   220       230       240       250       260       270       280
   TAGGAGACGGAACAACCGTTGATGAAGTTGTTGATGTTGTCGATGGCCTGGTTAATACCCTCGTTCAGCTTG
     | | |  ||| |  |  | || || |   ||            |  |||  | || |   |  |  |
   CTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGT
     310       320       330       340       350       360       370

 290       300       310       320       330       340         350
   GAGTTGATGTCGTTGAAGTCGATGTTAATGTTGGACTTCTCCTTCTCGGAGTA--GATGTTGTATCTGTACT
   ||  | || | |      |  | |  | |   | | |    |  |  |  |||   |  |  | || |
   GAAATCATCTGG--ACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGA
   380       390      400       410       420       430       440

 360       370       380       390       400        410       420      430
   TGATGATCTCCTCCAAAGCTTGGGCCTGGTAGTTCAAGGCCTTGTAC-ATACCCTCCTTGATGGTGTAGAAT
   | |  |||||   | |         ||||   |||    || |   | | |  |  ||  ||       ||
   TCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAA
   450       460       470       480       490       500       510

          440            450       460       470       480       490
   TGGGTGTTGACGG-----TGGACAACCATTGGGCGACGATCAAACCGTACATGTCGGACCACTTCTCGTTTC
   |     |  ||||     ||  | ||||     |||    ||| | |   |      ||   |
   TCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACA
 520       530       540       550       560       570       580       590

   500       510       520       530       540       550       560
   TCTTGGTCAAAGCGTTGTCGATGGTCTTGATGATCTTGTTCTTGTTGTCGATGTAGGACTCCAA-CAAGAAG
   || || |||||   | | || | ||| |||   ||     ||   | | |||  |  ||| ||| |     |
   TCATGTTCAAA--CTGGACGGTTGTCGTGACACTC-ACCGCTACATCTGGATCAAATACTTCAATCTGTTCG
         600       610       620          630       640       650       660

  570       580       590         600       610       620       630
   GCACCGACGACTGGGATCAACAACTCTGGGA--TGAACTCCAACAAGATGGAGGCACCAGCGATCTCGAAAG
    ||  ||       ||  || || ||   ||  || ||  |||| ||    |     | |  |||  |||||
   ACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAA---TTCTGGTATCCTGAAAG
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        670       680       690       700       710          720

640       650       660       670       680       690       700
 CGTTCTCGAAGTTACCCTTGGCGGTCTCGTTACCGACGTTCAAGGCCAAACCG-ATGTATGGGACAATCAAG
   |||| |        | ||  |  |     ||||   | || |   || | | |    | ||||  | |
 ACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACG
730      740       750       760       770       780       790       800

710      720          730         740       750       760       770
 GAGATGTCGGCAATCT---TGTCCATGGT--GTTGGACTTGTTAGCCTCGATGACGAAATCGTTGACGATCT
   || |||  |||| |   | |||  |||    || || ||  ||   ||             |||| | |
 TTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCA
       810       820       830       840       850       860       870

  780       790       800       810       820       830       840
 GCTTGACCCAACCAGCGAACAAACCGGCCTCGACG-ACCTTGTTAGCAGTCTTGATGTAGTCCATGGAGAAG
  | |    | ||| |    |   || |   ||  | |||   ||     ||  ||  ||  |    |  ||
 ACAT----CTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAAC
         880       890       900       910       920       930       940

 850       860       870       880       890       900       910
 AAGGAGTAGACCTTGTTGGAGAACAGCAGGGCGTCGTCGAAGGAAGAGGTCAAGGAGATGTCTCTGATGTCC
 |||||  | | | |     | ||     | |  |     || |  |  || ||| | |        ||  |
 AAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACA----AAGAATACCG
       950       960       970       980       990          1000

920       930       940       950       960       970       980       990
 AAAGGGAAGGTCTGAGAGTACAGGTATTGGA-AGATGGTGTTCTCGTCGGTGAAAATCTTCTTGATAGCTGG
    ||  |    ||    |   | |  || | | | | | || ||  |  || |||||          |  |
 TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATC-------CCGGACG
1010    1020      1030      1040      1050      1060             1070

       1000      1010      1020      1030      1040          1050
 TTGCTTCTCGTAGACTGGGACGTCGACGTTGAAGTCAGTCAAGGACTCGGTGTTC----TCGGATGGCAACT
 ||| |  ||     | || |  |  |   |||| ||    || |||  ||   ||     |  |||  || |
 TTGGTAATCTGTCTCAGGTAGTTGTA--ATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAAT
   1080      1090      1100        1110      1120      1130      1140

1060      1070      1080      1090      1100      1110      1120      1130
 CGATCTTGGAGATCAAGTCGGTGTCCAAGATCAACTCGTTGATTGGGAAGTCGTTCTCGATGTAGTTGGACT
   ||||    ||  |    |||  | |        || | | ||   |     |   | || | | |  |||
 GAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACT
   1150      1160      1170      1180      1190      1200      1210

        1140      1150      1160      1170      1180      1190      1200
 GGGTG-TTGTACTCGATTCTCTCGTTCTTGGACAAGTCGTCGGAGAAGGAGTTCTTGTCAGCGATGAAGAAC
 || || ||  |   | | |  ||||        | ||       | |     ||| |   ||  |   ||
 GGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCA----CTCTGGGTTGCTCTTGGGAGT
  1220      1230      1240      1250      1260         1270      1280

      1210          1220      1230      1240 X
 AAGTCCTCGTTGTCGAC----GTCGATACAGATTCCTGGAGCCAT
    |||  ||||  |||    |  |  |  |    ||| | ||
 TCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
    1290      1300      1310      1320      1330


2. US-09-910-186A-21' (1-1242)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    65  Optimized Score  =   457  Significance =  0.87
Residue Identity  =   42%  Matches          =   556  Mismatches   =   657
Gaps              =   108  Conservative Substitutions             =     0

                     X       10        20        30        40
                     TTAGAACATCTCGATCAAGATGGTGTCGTTGGTGTAGATG---GACAAGTCG
                      || | ||     ||||  |     ||  |  || |  ||    || | ||
 CTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCC
  20        30        40        50        60        70        80

 50        60           70        80        90       100            110
 AATGGCATGATGG---TCTTCAAGTACTTGTTGACCTTGGACTTCTCGTACTCAG------CGGAACCGATC
 |||  | |||| |   | |     |||   |  |   |  || ||   |    ||        || ||||||
 AATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATC
90      100       110       120       130       140       150       160

      120       130       140                    150       160
 AAGTACAACTTGTTCTCGTCGATGTAGTTCAA-------------CAAGTTCTTCTTCAGGGTGTTGTCG--
  |  | ||   | || |   | |  |  |  |              ||||| | ||  ||  || | |||
 GACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTA
  170       180       190       200       210       220       230

        170       180       190       200                      210
 ---------AAGTCCAACAACTTCTCGACGGCCAATGGAAT---------------CATCTTCTTCATCAAG
          | || | | |||||||| ||  ||    | ||               | ||  || ||||
 TACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
     240       250       260       270       280       290       300

 220       230       240       250       260       270       280
 TAGGAGACGGAACAACCGTTGATGAAGTTGTTGATGTTGTCGATGGCCTGGTTAATACCCTCGTTCAGCTTG
   | | |  ||| |  |  | || || |   ||            |  |||  | || |   |  |  |
 CTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGT
   310       320       330       340       350       360       370

290      300       310       320       330       340       350
 GAGTTGATGTCGTTGAAGTCGATGTTAATGTTGGACTTCTCCTTCTCGGAGTA--GATGTTGTATCTGTACT
 ||  | || | |      |  | |  | |   | | |    |  |  |  |||   |  |  | || |
 GAAATCATCTGG--ACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGA
 380       390       400       410       420       430       440

360      370       380       390       400        410       420       430
 TGATGATCTCCTCCAAAGCTTGGGCCTGGTAGTTCAAGGCCTTGTAC-ATACCCTCCTTGATGGTGTAGAAT
 | |  |||||   | |         ||||   |||    || |   | | |  |  ||  ||       ||
 TCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAA
 450       460       470       480       490       500       510

        440            450       460       470       480       490
 TGGGTGTTGACGG-----TGGACAACCATTGGGCGACGATCAAACCGTACATGTCGGACCACTTCTCGTTTC
 |     |  ||||     ||  | ||||     |||    ||| | |   |      ||   |
 TCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACA
520     530       540       550       560       570       580       590

 500       510       520       530       540       550       560
 TCTTGGTCAAAGCGTTGTCGATGGTCTTGATGATCTTGTTCTTGTTGTCGATGTAGGACTCCAA-CAAGAAG
 || || |||||   | | || | ||| |||   ||     ||   | | |||  |  ||| ||| |     |
 TCATGTTCAAA--CTGGACGGTTGTCGTGACACTC-ACCGCTACATCTGGATCAAATACTTCAATCTGTTCG
       600       610       620       630       640       650       660

 570      580        590         600       610       620       630
 GCACCGACGACTGGGATCAACAACTCTGGGA--TGAACTCCAACAAGATGGAGGCACCAGCGATCTCGAAAG
  ||  ||       ||  || ||   ||  || ||  |||| ||    |     | |  |||  |||||
 ACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAA---TTCTGGTATCCTGAAAG
         670       680       690       700       710          720

640       650       660       670       680       690       700
 CGTTCTCGAAGTTACCCTTGGCGGTCTCGTTACCGACGTTCAAGGCCAAACCG-ATGTATGGGACAATCAAG
   |||| |        | ||  |  |     ||||   | || |   || | | |    | ||||  | |
 ACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACG
730      740       750       760       770       780       790       800

710      720          730         740       750       760       770
 GAGATGTCGGCAATCT---TGTCCATGGT--GTTGGACTTGTTAGCCTCGATGACGAAATCGTTGACGATCT
   || |||  |||| |   | |||  |||    || || ||  ||   ||             |||| | |
 TTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCA
       810       820       830       840       850       860       870

  780       790       800       810       820       830       840
 GCTTGACCCAACCAGCGAACAAACCGGCCTCGACG-ACCTTGTTAGCAGTCTTGATGTAGTCCATGGAGAAG
  | |    | ||| |    |   || |   ||  | |||   ||     ||  ||  ||  |    |  ||
 ACAT----CTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAAC
         880       890       900       910       920       930       940

 850       860       870       880       890       900       910
 AAGGAGTAGACCTTGTTGGAGAACAGCAGGGCGTCGTCGAAGGAAGAGGTCAAGGAGATGTCTCTGATGTCC
 |||||  | | | |     | ||     | |  |     || |  |  || ||| | |        ||  |
 AAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACA----AAGAATACCG
```

```
        950       960       970       980       990          1000

 920       930       940       950       960       970       980       990
  AAAGGAAGGTCTGAGAGTACAGGTATTGGA-AGATGGTGTTCTCGTCGGTGAAAATCTTCTTGATAGCTGG
     ||  |    ||    |   | |  || | | | | | || ||  |  || |||||         |   |
  TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATC-------CCGGACG
1010      1020      1030      1040      1050      1060             1070

        1000      1010      1020      1030      1040          1050
  TTGCTTCTCGTAGACTGGGACGTCGACGTTGAAGTCAGTCAAGGACTCGGTGTTC----TCGGATGGCAACT
  ||| |  ||     | || |  |  |   |||| ||    || |||  ||   ||     |  |||  || |
  TTGGTAATCTGTCTCAGGTAGTTGTA--ATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAAT
    1080      1090      1100         1110      1120      1130      1140

 1060      1070      1080      1090      1100      1110      1120      1130
  CGATCTTGGAGATCAAGTCGGTGTCCAAGATCAACTCGTTGATTGGGAAGTCGTTCTCGATGTAGTTGGACT
    ||||    ||  |    |||  | |        || | | ||   |     |   | || | | |  |||
  GAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACT
    1150      1160      1170      1180      1190      1200      1210

           1140      1150      1160      1170      1180      1190      1200
  GGGTG-TTGTACTCGATTCTCTCGTTCTTGGACAAGTCGTCGGAGAAGGAGTTCTTGTCAGCGATGAAGAAC
  || || ||  |   | | |  ||||        | ||       | |     ||| |   ||  |   ||
  GGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCA----CTCTGGGTTGCTCTTGGGAGT
  1220      1230      1240      1250      1260            1270      1280

         1210           1220      1230      1240 X
  AAGTCCTCGTTGTCGAC----GTCGATACAGATTCCTGGAGCCAT
     |||  ||||  |||    |  |  |  |    ||| | ||
  TCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
    1290      1300      1310      1320      1330


3. US-09-910-186A-21' (1-1242)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    61  Optimized Score   =    448  Significance = -0.87
Residue Identity  =    39%  Matches           =    519  Mismatches   =   713
Gaps              =    68  Conservative Substitutions             =     0

                      X         10        20        30        40        50
                      TTAGAACATCTCGATCAAGATGGTGTCGTTGGTGTAGATGGACAAGTCGAAT
                      ||   | |||  || ||| ||   |   ||  |    ||       |  |    |||
  ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAAT
          10        20        30        40        50        60        70

         60        70        80        90       100       110       120
  GGCATGATGGTCTTCAAGTACTTGTTGACCTTGGACTTCTCGTACTCAGCGGAACCGATCAAGTACAACTTG
     ||     | |     |||      |   | ||  | |   ||   |  |||| ||   |  | |||  |
  CTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAG
         80        90       100       110       120       130       140

     130       140       150       160       170       180       190
  TTCTCGTCGATGTAGTTCAACAAGTTCTTCTTCAGGGTGTTGTCGAAGTCCAACAACTTCTCGACGGCC---
  |||     ||  |  | |   || |      || | ||      |||    |||| | |||  |   ||
  TTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTA
     150       160       170       180       190       200       210

         200       210         220       230       240       250       260
  --AATGGAATCATCTTCTTCATCAAG--TAGGAGACGGAACAACCGTTGATGAAGTTGTTGATGTTGTCGAT
      |||| |  |||  ||| |   |  |  |   |   | |  |    | || | | |  |   |  |
  TTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATC
   220       230       240       250       260       270       280

         270       280         290       300       310       320       330
  GGCCTGGTTAATACCCTCGT--TCAGCTTGGAGTTGATGTCGTTGAAGTCGATGTTAATGTTGGACTTCTCC
    |   |   | ||| || |   | || || ||   |  ||      |  ||| |  ||    |    |
  CACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGT
 290       300       310       320       330       340       350       360

         340       350       360       370       380       390       400
  TTCTCGGAGTAGATGTTGTATCTGTACTTGATGATCTCCTCCAAAGCTTGGGCCTGGTAGTTCAAGGCCTTG
   ||     |    || |  || |  ||   | ||      ||||| ||     ||   | | |||   |
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  ATCATCTGGACTCTGATCGATATCAACGGTAAGA------CCAAATCTGTATTCTTCGAATACAACATCCGT
       370       380       390             400       410       420

     410       420       430       440       450           460       470
  TACATACCCTCCTTGATGGTGTAGAATTGGGTGTTGACGGTGGACAACCAT----TGGGCGACGATCAAACC
   |      |||        |  |    ||| | ||         || | ||    ||  | | | | ||| |
  GAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATC
   430       440       450       460       470       480       490

       480         490       500          510       520       530
  GTACATGTCGGACCACT--TCTCGTTTCTCTTGGTCAAAG-CGTTGTCGATGGTCTTGATGATCTTG--TTC
          |||   |||    ||   |  |    |||||| | |    || | | | | | |   ||   ||
  TACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATC
 500       510       520       530       540       550       560       570

 540       550       560       570       580       590       600       610
  TTGTTGTCGATGTAGGACTCCAACAAGAAGGCACCGACGACTGGGATCAACAACTCTGGGATGAACTCCAAC
   | ||     || | |    || | |     | | |   |   |||| ||  |||     ||   |  || |
  ATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACC
         580       590       600       610       620       630       640

         620       630       640       650       660       670       680
  AAGATGGAGGCACCAGCGATCTCGAAAGCGTTCTCGAAGTTACCCTTGGCGGTCTCGTTACCGACGTTCAAG
   |  ||       |    |||    ||  || |  ||      | |   | |  |   |       |||  |
  GAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGG
     650       660       670       680       690       700       710

     690       700       710       720       730       740       750
  GCCAAACCGATG-TATGGACAATCAAGGAGATGTCGGCAATCTTGTCCATGGTGTTGGACTTGTTAGCCTC
  |  || ||| || | |   ||||  ||    || |   ||||  ||   |       | |||  |    |
  GGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAA----CAAGAACTCTTACATCAA
    720       730       740       750       760           770       780

    760       770             780       790       800       810
  GATGACGAAATCGTTGACGATCTG------CTTGACCCAACCAGCGAACAAACCGGCCTCGACGACCTTGTT
    ||| ||||   |   || |  |      | |||| |   |     |||| | |  ||| |    | |
  ACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAA
     790       800       810       820       830       840       850

 820       830       840                 850       860       870
  AGCAGTCTTGATGTAGTCCATGGAGAAG--------AAGGAGTAGACCT-TGTTGGAGAACAGC----AGGG
        |    ||||   |   || |||          |  | | | ||   |   ||  || |    | |
  CTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGA
    860       870       880       890       900       910       920

 880         890       900            910                920       930
  CGTCGT--CGAAGGAAGAGGTCAAGGA----GATGTCT-----CTGATGTCCAAAGGGAAGGTCTGAGAGTA
  | ||||    || |||||   ||   |    ||  |||     ||||      || ||   || |     ||
  CATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTA
   930       940       950       960       970       980       990

 940       950       960       970       980       990      1000      1010
  CAGGTATTGGAAGATGGTGTTCTCGTCGGTGAAAATCTTCTTGATAGCTGGTTGCTTCTCGTAGACTGGGAC
  || ||| |  ||||  |          | |     |      |||  ||| || |  |            ||
  CAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACAC
1000      1010      1020      1030      1040      1050      1060      1070

      1020      1030      1040      1050      1060      1070      1080
  GTCGACGTTGAAGTCAGTCAAGGACTCGGTGTTCTCGGATGGCAACTCGATCTTGGAGATCAAGTCGGTGTC
        | | ||   |  | | ||   |  |  ||    | || |   | | ||  |||   |    |  ||
  CATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATC
      1080      1090      1100      1110      1120      1130      1140

     1090      1100      1110      1120      1130              1140
  CA-AGATCAACTCG--TTGATTGGGA-AGTCGTTCTCGATGTAGTTGGACTGGGTGTTG-----TACTCGAT
   |  ||  || |||   |||| || |    |  | || | | |  |||  | |   | |     |||
  TACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACAAAGA
     1150      1160      1170      1180      1190      1200      1210

 1150      1160      1170      1180      1190      1200      1210
  TCTCTCGTTCTTGGACAAGTCGTCGGAGAAGGAGTTCTTGTCAGCGATGAAGAACAAGTCCTCGTTGTCGAC
     ||  | | |   ||| | ||    ||||||  |            | | |||  |     |   |  |
  CTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTGCAA
```

```
    1220      1230      1240      1250      1260      1270      1280

1220      1230      1240 X
  GTCGATACAGATTCCTGGAGCCAT
   | |      || ||   || |
  TTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAAC
  1290      1300      1310      1320      1330
```

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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-22.res made by bobryen on Thu 7 Nov 102 14:35:52-PST.

Query sequence being compared:US-09-910-186A-22 (1-413)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-22 (1-413) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -  *
N     -
C     -
E     -                                                          *
S    0-----------------------------------------------------------------
      |     ||     |      |     |      |     ||     |      |     |
SCORE 0     46     92    137   183   229    275   320    366   412
STDEV       0                                1

                              PARAMETERS

Similarity matrix      PAM-150     K-tuple                       1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty              20
Gap penalty               5.00     Window size                 413
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                          151          21       225.75

Times:                     CPU                  Total Elapsed
                      00:00:00.00               00:00:00.00

Number of residues:                   1704
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                     Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                        ****  1 standard deviation above mean ****
   1. US-08-123-975A-2 Sequence 2, Application U    850   412   412   1.16   0
                        ****  0 standard deviation from mean ****
   2. US-08-123-975A-3 Sequence 3, Application U    415    22   185  -0.57   0
   3. US-08-123-975A-5 Sequence 5, Application U    439    20   184  -0.58   0

1. US-09-910-186A-22 (1-413)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    412  Optimized Score  =    412  Significance =  1.16
Residue Identity =   100%  Matches          =    412  Mismatches   =     0
Gaps             =      0  Conservative Substitutions             =     0

     X      10        20        30        40        50        60        70
    MAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLT
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
     APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLT
     X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    DFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANKV
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    DFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANKV
           80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    VEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFIP
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    VEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFIP
        150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    ELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQ
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALNYQAQ
      220       230       240       250       260       270       280

   290       300       310       320       330       340       350       360
    ALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKLLDFDN
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKLLDFDN
    290       300       310       320       330       340       350

           370       380       390       400       410  X
    TLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMF
    |||||||||||||||||||||||||||||||||||||||||||||||||||||
    TLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKD
  360       370       380       390       400       410 X     420       430

    N


2. US-09-910-186A-22 (1-413)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =     22  Optimized Score  =    185  Significance = -0.57
Residue Identity =     8%  Matches          =     37  Mismatches   =   342
Gaps             =      3  Conservative Substitutions             =    31

         X       10        20        30        40        50        60
         MAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSEN
                                          |         |    | :         |  |
    RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
         X  10        20        30        40        50        60        70

     70        80        90       100       110       120       130
    TESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIK
```

```
              :       :  |:      |   |                    :      ::
    NSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLN
          80        90       100       110       120       130       140

  140       150       160       170       180       190       200       210
    TANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASIL
     :   : : |                |    :|   |    :      |       |   :     : : ||
    NSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
       150       160       170       180       190       200       210

          220       230       240       250       260       270       280
    LEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKAL
     :|  : |      ::|  |  ||   :  :     :         | :           :   |    |
    KDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVG---IRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYA
     220       230       240          250       260       270       280

        290       300       310       320       330       340       350
    NYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKL
                  |     | |                     |  : |              |
    SGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMN
      290       300       310       320       330       340       350

      360       370       380       390       400       410  X
    LDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMF
    |   |        :   |      ::      : :  :|       |   |
    LQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
    360       370       380       390       400       410    X


3. US-09-910-186A-22 (1-413)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     20  Optimized Score  =    184  Significance = -0.58
Residue Identity =    11%  Matches          =     50  Mismatches   =   327
Gaps             =     32  Conservative Substitutions              =    32

    X       10        20        30        40            50        60
    MAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIEND----FPINELILDTDLISKIELPSENT
              |  |      |   |      ::|        :                     |   |
    FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFL
    X       10        20        30        40        50        60        70

    70        80        90       100       110       120       130       140
    ESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKT
    :    | : :| |        |  :   |            ||         |       |  ||
    DFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSV--FFEYNIRED
          80        90       100       110       120       130         140

           150       160       170       180       190
    ANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNF-------------
        :    |        |  :    |      | ||  ::           :  :  |
    ISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTEL
         150       160       170       180       190       200       210

        200       210       220       230       240       250       260
    ------ENAFEIAGASILLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWL
          |     : :  | :|    |      ::  :   |     |                    :
    SQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRD
       220       230       240       250       260       270       280

      270       280       290       300       310       320              330
    STVNTQFYTIKEGMYKALNYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKL-------NEGINQAIDN
      :   |   :     : |      |: |   :       :      |     ||        :     |
    LYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQI
     290       300       310       320       330       340       350

           340       350       360       370       380       390       400
    INNFINGCSVSYLMKKMIPLAVEKLLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSI
                |: |    : :                 :| | |   |  | |    |     :
    KEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQF
   360       370       380       390       400       410       420       430

         410
```

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YTNDTILIEMF
   |    |
IPKDEGWTE
        X
```

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O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-23.res made by bobryen on Thu 7 Nov 102 14:47:57-PST.


Query sequence being compared:US-09-910-186A-23 (1-1200)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-23 (1-1200) with:
        File : US08123975A.seq

    100-
       -
N      -
U   50-
M      -
B      -
E      -
R      -
       -
O      -
F   10-
       -
S      -
E    5-
Q      -
U      -
E      -                                               *
N      -
C      -
E      -                                                             *
S    0----------------------------------------------------------------------
      ||     |  |   |   |  |    | |     ||      |      ||     | |    |
SCORE 0|    10  |  20   | 30     |40    51     61     71|    81 |   91
STDEV -6       -5      -4      -3      -2      -1       0       1


                        PARAMETERS

Similarity matrix       Unitary    K-tuple                   4
Mismatch penalty              1    Joining penalty          30
Gap penalty                5.00    Window size             500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                     SEARCH STATISTICS

Scores:                  Mean        Median      Standard Deviation
                          77          72           11.55

Times:                 CPU                       Total Elapsed
                    00:00:00.00                  00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351    91   406   1.21   0
                    ****  0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338    71   304  -0.52   0
  3. US-08-123-975A-1 Sequence 1, Application U   1338    71   304  -0.52   0


1. US-09-910-186A-23 (1-1200)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    91  Optimized Score   =   406  Significance =  1.21
Residue Identity =    42%  Matches           =   492  Mismatches   =   571
Gaps              =   100  Conservative Substitutions          =     0
                      X       10        20        30        40        50
                      ATGTCCCTGTACAACAAGACCCTTGACTGTAGAGAGCTGCTGGTGAAGAACA
                      ||  |    ||||| ||   |  |  |   |   |  | |      |  |||
  CTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACA
230       240       250       260       270       280       290       300

        60        70        80        90       100       110       120
  CTGACCTGCCATTCATCGGTGACATCAGTGACGTGAAGACTGACATCTTCCTGCGTAAGGACATCAACGAGG
  |   | |    | |||     | | |  ||    |||||    |  | |||   ||||    |||| |  |
  CCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGA---TCTCCATCCGCGGTAACCGTATCATCTGGA
        310       320       330       340          350       360       370

     130       140       150       160       170       180       190
  AGACTGAGGTGATCTACTACCCAGACAACGTGTCAGTAGACCAAGTGATCCTCAGTAAGAACACCTCCGA--
          |  ||| ||        |||      | |   | ||   | | || || |  ||| ||| ||
  CTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAAT
         380       390       400       410       420       430       440

     200       210       220           230       240         250       260
  GCATGGACAACTAGACCTGCTCTACC----CTAGTATCGACAGTGAGAGTGAGATC--CTGCCAGGGGAGAA
   |||  |   || |  || |  ||||    | | || |   |   |   | | |||  |  | | || | |
  ACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAAC
       450       460       470       480       490       500       510

                   270       280       290       300       310       320
  TCAAGTCT----------TCTACGACAACCGTACCCAGAACGTGGACTACCTGAACTCCTACTACTACCTAG
  |  | |||          || | |||| ||||      | ||   ||    |||| || | || | | || |
  TGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAAC--GGTGAAATCAT-CTTCAAACTGG
     520       530       540       550       560         570        580

       330            340       350       360       370        380
  AGTCTCAGAAGCTGAGT-----GACAACGTGGAGGACTTCACTTTCACGCGTTCA-ATCGAGGAGGCTCTGG
  |   | | |      ||     |   |  |||| ||  |   | ||   | |  | | |||   | ||| |
  ACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGT
      590       600       610       620       630       640       650

 390       400        410       420       430       440       450
  ACAACAGTGCAAAGGTGTAC-ACTTACTTCCCTACCCTGGCTAACAAGGTGAATGCCGGTGTGCAAGGTGGT
   ||| |  | | |   |||| |  | |   | ||| | |  || |     || | | ||          |||
  CCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGG----------GGT
    660       670       680       690       700       710

460       470       480       490       500       510       520       530
  CTGTTCCTGATGTGGGCAAACGACGTGGTTGAGGACTTCACTACCAACATCCTGCGTAAGGACACACTGGAC
        |||||||     || ||      |  |  |    ||   ||||       | |   || |||| |
  AATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAG
  720       730       740       750       760       770       780

        540       550       560            570       580        590
  AAGATCTCAGATGTGTCAGCTATCATCCC-----CTACATCGGACCCGCACTGAACAT-CTCCAACT-----
  ||   |||    ||    |  ||| |  |     | | ||   ||| | |||  | || |  |||||
  AAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGC
790       800       810       820       830       840       850       860

          600       610       620       630       640       650       660
  ---CTGTGCGTCGTGGAAACTTCACTGAGGCATTCGCAGTCACTGGTGTCACCATCCTGCTGGAGGCATTCC
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       |||| | |||  ||||  |   | |  |  |||||        | |||         ||  | |||  |
    GACCTGTACATCGGTGAAAAGTTCATCA-TCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACAT--C
           870       880       890       900       910       920         930

          670       680       690       700       710       720       730
    CTGAGTTCACAATCCCTGCTCTGGGTGCATTCGTGATCTACAGTAAGGTCCAGGAGCGAAACGAGATCATCA
     |  ||  | ||  |    |||   || |  | |  || ||   ||     |   |||     | | |  ||
    GTACGTAAAGAAGACTACATCTACCTGGA--CTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACA
           940       950         960       970       980       990      1000

        740       750       760       770       780       790       800
    AGACCATCGACAACTGTCTGGAGCAGAGGATCAAGAGATGGAAGGACTCCTACGAGTGGATGATGGGAACGT
    ||  | || | ||        || ||| ||  ||    |     | |||| |    ||  |     ||||
    AGTACTTCAAGAA--------AGAAGAAGA--AAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAAC--
          1010              1020        1030      1040      1050      1060

       810       820       830       840       850       860       870
    GGTTGTCCAGGATCATCACCCAGTTCAACAACATCTCCTACCAGATGTACGACTCCCTGAACTACCAGGCAG
           |   | || || |||| ||||  |   |  | | |||  |  | ||||     |    |
    ------TCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGC-----T
                1070      1080      1090      1100      1110      1120

    880       890       900       910       920       930       940
    GTGCAATCAAGGCTAAGATCGACCTGGAGTACAAGAAGTACTCCGGAAGCGACAAGGAGAACATCAAGAGCC
    || |||  |||   ||||     |||  | |   |   |  || | |  |  |            | ||  |
    GTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACC------GTTTCTACGAATC
          1130      1140      1150      1160      1170            1180

   950       960       970       980       990      1000      1010      1020
    AGGTTGAGAACCTGAAGAACAGTCTGGACGTCAAGATCTCGGAGGCAATGAACAACATCAACAAGTTCATCC
     |||   | |   |||||| |      | | | |  |||      | |      || | ||  |  | |  |
    TGGTATCGTATTCGAAGAATA----CAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAAC
   1190      1200          1210      1220      1230      1240      1250

          1030      1040      1050      1060      1070      1080      1090
    GAGAGTGCTCCGTCACCTACCTGTTCAAGAACATGCTGCCTAAGGTCATCGACGAGCTGAACGAGTTCGACC
    |  |    | |  |    | |||      ||   || |   |     |  |||||         ||| ||||
    GCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGA-------AGGTTGGACC
     1260      1270      1280      1290      1300      1310              1320

        1100      1110      1120  X   1130      1140
    GAAACACCAAGGCAAAGCTGATCAACCTGATCGACTCCCATAACATCATCC
    |||     |   | |   |      |   |
    GAATAGTAACCTCTAGAGTCGAGGCCTGCAG
          1330      1340      1350

2. US-09-910-186A-23 (1-1200)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     71  Optimized Score  =    304  Significance = -0.52
Residue Identity =    43%  Matches          =    365  Mismatches   =   401
Gaps             =     71  Conservative Substitutions               =     0

         370       380  X    390       400       410       420       430
    CACGCGTTCAATCGAGGAGGCTCTGGACAACAGTGCAAAGGTGTACACTTACTTCCCTACCCTGGCTAACAA
                        ||| | ||    |     | |||  || | |        | |    ||||
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

        440       450       460       470       480       490       500
    GGTGAATGCCGGTGTGCAAGGTGGTCTGTTCCTGATGTGGGCAAACGACGTGGTTGAGGACTTCACTACCAA
      | ||| ||    |          |||  ||||   |  | |  | |     |    ||| |  ||  | |
    CATCAATACCTCCAT---------CCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTA
          60                  70        80        90       100       110

      510       520       530       540       550       560       570
    CATCCTGCGTAAGGACACACTGGACAAGATCTCAGATGTGTCAGCTATCATCCCCTACATCGGACCCGCACT
    |   || |  ||    |||  ||             |     || || | ||      ||| || |  ||
    C--GCTTCCAAAATCAACATCGG-------------TTCTAAAGTTAACTTC-----GATCCGATCGACAAG
        120       130                    140       150             160

    580       590       600       610             620       630       640
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    GAACATCTCCAACTCTGTGCGTCGTGGAAACTTC----ACTGAGGCATTCGCAGTCACTGGTGTCACCATCC
     | ||  ||||   |||| |    ||||| ||||    |  || |   ||      | || | ||   || |
    AATCAGATCCA--GCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATC-GTATAC
    170         180       190       200       210       220       230

     650       660       670       680       690        700       710
    TGCTGGAGGCATTCCCTGAGTTCACAATCCCTGCTCTGGGTGCAT-TCGTGATCTACAGTAAGGTCCAGGAG
      ||  | |  | |    | ||| | | ||    ||||| | | | ||  ||  |||   ||   |
    AACTCTATG--TACGAAAACTTCTCCA-CCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
     240         250       260        270       280       290       300

    720       730       740       750       760       770       780
    CGAAACGAGATCATCAAGACCATCGACAACTGTCTGGAGCAGAGGATCAAGAGATGGAAGGACTCCTACGAG
    |  |||   |      | ||||||  ||||||  ||||  | |  ||   |    | ||| |   ||
    CTGAAC---AATGAATACACCATCATCAACTGCATGGA--AAACAATTCTGGTTGGAAAGTATCTCTGAACT
      310          320       330       340         350       360       370

   790       800       810       820       830                    840      850
    TGGATGATGGGAACGTGGTTGTCCAGGATCATCACCCAGTTCAACA-----------ACATCTCCTACCAGA
      | |||    | |  |  | | |||||   |||   | |  ||||            ||  | ||  ||||
    ACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
        380       390       400       410       420       430       440

           860       870       880       890       900       910       920
    TGTACGACTCCCTGAACTACCAGGCAGGTGCAATCAAGGCTAAGATCGACCTGGAGTACAAGAAGTACTCCG
    ||  | ||  |    |||||       |    |||   | ||  |||  |    |      |||  |||||
    TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCA
       450       460       470       480       490       500       510

         930       940       950       960       970       980       990
    GAAGCGACAAGGAGAACATCAAGAGCCAGGTTGAGAACCTGAAGAACAGTCTGGACGTCAAGATCTCGGAGG
     || | |||   |   |     || |   |   |||| | ||    || ||||   |  || |||   |
    AAATCTACATCAACGGCCGTCTGATC---GACCAGAAACCGATCTCCAATCTG---GGTAACATCCACGCTT
     520       530       540            550       560        570       580

      1000      1010      1020         1030      1040      1050      1060
    CAATGAACAACATCAACAAGTTCATCCGAGAGTG---CTCCGTCACCTACCTGTTCAAGAACATGCTGCCTA
    | |  |||| |||   |||  |   | |     |   | |   |  |||| | |  |  ||     |   |
    CTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATC
      590       600       610       620       630       640       650

       1070      1080      1090      1100      1110      1120      1130
    AGGTCATCGACGAGCTGAACGAGTTCGACCGAAACACCAAGGCAAAGCTGATCAACCTGATCGACTCCCATA
     | ||  | | || |||||      |||   | | | ||| |    |     ||||| |  | | ||   ||
    TGTTCGACAAAGAACTGAA------CGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
       660       670             680       690       700       710       720

     1140      1150      1160      1170      1180      1190      1200
    ACATCATCCTGGTCGGTGAGGTCGACAAGCTGAAGGCAAAGGTAAACAACAGCTTCCAGAACTAA
     | | |      || | |  | | ||  || | | |  ||     || |||   |  |    ||
    TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
           730       740       750       760       770       780     X 790

    ACAAATACGTTGA
         800

3. US-09-910-186A-23 (1-1200)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     71  Optimized Score  =    304  Significance = -0.52
Residue Identity =    43%  Matches          =    365  Mismatches   =   401
Gaps             =     71  Conservative Substitutions               =     0

         370       380  X    390       400       410       420       430
    CACGCGTTCAATCGAGGAGGCTCTGGACAACAGTGCAAAGGTGTACACTTACTTCCCTACCCTGGCTAACAA
                        ||| | ||    |     | |||  || | |        | |    ||||
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

        440       450       460       470       480       490       500
    GGTGAATGCCGGTGTGCAAGGTGGTCTGTTCCTGATGTGGGCAAACGACGTGGTTGAGGACTTCACTACCAA
      | ||| ||    |          |||  ||||   |  | |  | |     |    ||| |  ||  | |
  CATCAATACCTCCAT---------CCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTA
        60                 70        80        90       100       110

   510       520       530       540       550       560       570
  CATCCTGCGTAAGGACACACTGGACAAGATCTCAGATGTGTCAGCTATCATCCCCTACATCGGACCCGCACT
  |   || |  ||    |||  ||             |     || || | ||      ||| || |  ||
  C--GCTTCCAAAATCAACATCGG-------------TTCTAAAGTTAACTTC-----GATCCGATCGACAAG
      120       130                    140       150            160

 580       590       600       610           620       630       640
  GAACATCTCCAACTCTGTGCGTCGTGGAAACTTC----ACTGAGGCATTCGCAGTCACTGGTGTCACCATCC
   | ||  ||||   |||| |    ||||| ||||    |  || |   ||      | || | ||   || |
  AATCAGATCCA--GCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATC-GTATAC
  170         180       190       200       210       220       230

   650       660       670       680       690        700       710
  TGCTGGAGGCATTCCCTGAGTTCACAATCCCTGCTCTGGGTGCAT-TCGTGATCTACAGTAAGGTCCAGGAG
    ||  | |  | |    | ||| | | ||    ||||| | | | ||  ||  |||   ||   |
  AACTCTATG--TACGAAAACTTCTCCA-CCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCT
   240         250       260        270       280       290       300

  720       730       740       750       760       770       780
  CGAAACGAGATCATCAAGACCATCGACAACTGTCTGGAGCAGAGGATCAAGAGATGGAAGGACTCCTACGAG
  |  |||   |      | ||||||  ||||||  ||||  | |  ||   |    | ||| |   ||
  CTGAAC---AATGAATACACCATCATCAACTGCATGGA--AAACAATTCTGGTTGGAAAGTATCTCTGAACT
    310          320       330       340         350       360       370

790       800       810       820       830                  840       850
  TGGATGATGGGAACGTGGTTGTCCAGGATCATCACCCAGTTCAACA-----------ACATCTCCTACCAGA
    | |||    | |  |  | | |||||   |||   | |  ||||            ||  | ||  ||||
  ACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
       380       390       400       410       420       430       440

         860       870       880       890       900       910       920
  TGTACGACTCCCTGAACTACCAGGCAGGTGCAATCAAGGCTAAGATCGACCTGGAGTACAAGAAGTACTCCG
  ||  | ||  |    |||||       |    |||   | ||  |||  |    |      |||  |||||
  TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCA
     450       460       470       480       490       500       510

       930       940       950       960       970       980       990
  GAAGCGACAAGGAGAACATCAAGAGCCAGGTTGAGAACCTGAAGAACAGTCTGGACGTCAAGATCTCGGAGG
   || | |||   |   |     || |   |   |||| | ||    || ||||   |  || |||   |
  AAATCTACATCAACGGCCGTCTGATC---GACCAGAAACCGATCTCCAATCTG---GGTAACATCCACGCTT
   520       530       540          550       560          570       580

    1000      1010      1020         1030      1040      1050      1060
  CAATGAACAACATCAACAAGTTCATCCGAGAGTG---CTCCGTCACCTACCTGTTCAAGAACATGCTGCCTA
  | |  |||| |||   |||  |   | |     |   | |   |  |||| | |  |  ||     |   |
  CTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATC
       590       600       610       620       630       640       650

     1070      1080      1090      1100      1110      1120      1130
  AGGTCATCGACGAGCTGAACGAGTTCGACCGAAACACCAAGGCAAAGCTGATCAACCTGATCGACTCCCATA
   | ||  | | || |||||      |||   | | | ||| |    |     ||||| |  | | ||   ||
  TGTTCGACAAAGAACTGAA------CGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTA
     660       670             680       690       700       710       720

   1140      1150      1160      1170      1180      1190      1200
  ACATCATCCTGGTCGGTGAGGTCGACAAGCTGAAGGCAAAGGTAAACAACAGCTTCCAGAACTAA
   | | |      || | |  | | ||  || | | |  ||     || |||   |  |    ||
  TCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGA
         730       740       750       760       770       780    X  790

  ACAAATACGTTGA
       800
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> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-23-inv.res made by bobryen on Thu 7 Nov 102 14:48:11-PST.

Query sequence being compared:US-09-910-186A-23' (1-1200)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-23' (1-1200) with:
        File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                        *
S    0----------------------------------------------------------------------
      |      |      |  |    |      |      |    ||       |      |     ||
SCORE 0      8     16  |  24     32     41   |49      57     65     73
STDEV                 -1                       0                     1


                           PARAMETERS

Similarity matrix       Unitary      K-tuple                 4
Mismatch penalty              1      Joining penalty        30
Gap penalty                5.00      Window size           500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                         SEARCH STATISTICS

Scores:                   Mean         Median        Standard Deviation
                           58            29             25.98

Times:                 CPU                         Total Elapsed
                    00:00:00.00                     00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                            Init. Opt.
Sequence Name       Description                       Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U       1338    73   449   0.58   0
   2. US-08-123-975A-1 Sequence 1, Application U       1338    73   449   0.58   0
                   ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U       1351    28   440  -1.15   0


1. US-09-910-186A-23' (1-1200)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     73  Optimized Score     =   449  Significance =  0.58
Residue Identity  =    42%  Matches             =   527  Mismatches   =   653
Gaps              =     62  Conservative Substitutions                =     0

                        X       10        20        30        40        50
                        TTAGTTCTGGAAGCTGTTGTTTACCTTTGCCTTCAGCTTGTCGACCTCACCG
                         ||  ||  |||  |  |   |||||    | | | | ||     |  | |
    CTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCC
     20        30        40        50        60        70        80

          60        70        80        90      100       110       120
    ACCAGGATGATGTTATGGGAGTCGATCAGGTTGATCAGCTTTGCCTTGGTGTTTCGGTCGAACTCGTTCAGC
    |      ||||   |   |  ||| | | | |    |  |   | | |||  |   ||  |  ||| || |
    AATCACCTGAT-CGACCTGTCTCGCT-ACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
   90       100        110        120       130       140       150

       130       140          150       160       170       180       190
    TCGTCGATGACCTTAGGCAGCATGT---TCTTGAACAGGTAGGTGACGGAGCACTCTCGGATGAACTTGTTG
    ||| | |  | |  |  ||||   |   ||| |||           || ||   || | || |||     |
    TCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC-CTGAAGAATGCTATC
  160       170       180       190       200       210        220       230

        200       210       220       230       240       250       260
    ATGTTGTTCATTGCCTCCGAGATCTTGACGTCCAGACTGTTCTTCAGGTTCTCAACCTGGCTCTTGATGTTC
     | |    |  |   | ||| | |||  |  ||    | |   || |  || | |  |   ||       ||
    GTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATC
           240       250       260       270       280       290       300

      270       280       290       300       310       320       330
    TCCTTGTCGCTTCCGGAGTACTTCTTGTACTCCAGGTCGATCTTAGCCTTGATTGCACCTGCCTGGTAGTTC
    ||  ||     |    |   | || |  ||| || |   | |  |  || | | | |  |  ||   |  |
    TCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAAC-AATTCTGGTTGGAAAGTATCTCTGAACTA
         310       320       330       340        350       360       370

    340       350             360       370       380       390       400
    AGGGAGTCGTACATCTG------GTAGGAGATGTTGTTGAACTGGGTGATGATCCTGGACAACCACGTTCCC
     ||        ||||||      | |||| |    |   | |     |    |  |   |||  ||  ||
    CGG--TGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAG
          380       390       400       410       420       430       440

        410       420       430       440       450       460       470
    ATCATCCACTCGTAGGAGTCCTTCCATCTCTTGATCCTCTGCTCCAGACAGTTGTCGATGGTCTTGATGATC
    || ||| ||   |  || | | || ||| || |||| ||    ||  |       | || ||| |||  | |
    ATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACC--ATCACCAACAATCGTC-TGAATAAC
        450       460       470       480         490       500        510

      480       490       500       510       520       530       540
    TCGTTTCGCTCCTGGACCTTACTGTAGATCACGAATGCACCCAGAGCAGGGATTGTGAACTCAGGGAATGCC
    ||      || |   | |   |    ||||    |   ||| |   |     | |  |||        | |
    TCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCT
         520       530       540       550       560       570       580

    550       560       570       580       590       600       610
    TCCAGCAGGATGGTGACACCAGTGACTGCGAATGCCTCAGTGAAGTTTCCACGACGCACAGAGTTGGAGATG
       | ||  ||| | | ||  |    |     || | |       |      |   || | | ||  |  ||
    AATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTG
       590       600       610       620       630       640       650

  620       630       640       650       660       670        680       690
    TTCAGTGCGGGTCCGATGTAGGGGATGATAGCTGACACATCTGAGATCTTGTCC-AGTGTGTCCTTACGCAG
    |||      |  | ||   |       ||    |||   |  || | |  |||| | | ||   |   | |
  TTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAA
   660       670       680       690       700       710       720

          700       710       720                   730       740       750
  GATGTTGGTAGTGAAGTCCTCAACCACGTC----------GTTTGCCCA--CATCAGGAACAGACCACCTTG
  ||  |  |  ||||   |||  |  ||| |             |||  |  |   | || | || ||  |
  GACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATAC
 730       740       750       760       770       780       790       800

          760       770       780         790       800       810
  CACACCGGCATTCACCTTGTTAGCCAGGGT---AGGGAAGTAAGTGTACACCTTTGCACTGTTGTCCAGAGC
       || ||   |  | | || ||  |||   | | |  | |  |  |  | | |  ||||| |    | |
  GTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACC
          810       820       830       840       850       860       870

820        830       840       850        860       870       880
  CTCCTCGA-TTGAACGCGTGAAAGTGAAGTCCT-CCACGTTGTCACTCAGCTTCTGAGACTCTAGGTAGTAG
    | || |  ||||| | |    ||   ||  | |||  ||     |||     |  |  ||| |  |  ||
  AACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAG
       880       890       900       910       920       930       940

890           900       910       920       930       940       950
  TAGGA----GTTCAGGTAGTCCACGTTCTGGGTACGGTTGTCGTAGAAGACTTGATTCTCCCCTGGCAGGAT
   |  |    ||||         |   | |    |    ||| ||||   |    |       | | | || |
  GACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCT
     950       960       970       980       990      1000      1010

  960       970       980       990      1000            1010      1020
  CTCACTCTCACTGTCGATACTAGGGTAGAGCAGGTCTAGTTGTCCATG---CTCGGAGGTGTTCTTACTGAG
    || |    ||    |  || | |||||  || ||| ||   |  ||    ||   |  |||  || |  |
  ACCAAT---GCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTG
  1020         1030      1040      1050      1060      1070      1080

  1030       1040      1050      1060      1070      1080      1090
  GATCA-CTTGGTCTACTGACA-CGTTGTCTGGGTAGTAGATCACCTCAGTCTCCTCGTTGATGTCCTTACGC
    |||  | | | || ||| | |   |   |   ||   |||||       | |    |||      |  ||
  TCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGA-----ATCTGC
   1090      1100      1110      1120      1130      1140          1150

  1100      1110      1120      1130      1140      1150          1160
  AGGAAGATGTCAGTCTTCACGTCACTGATGTCACCGATGAATGGCAGGTCAGTGTT----CTTCACCAGCAG
  ||||  |   || |  | |||  |  | | ||| || |      ||| |||    |    ||  ||  |  |
  AGGACAA---CAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTG
         1160      1170      1180      1190      1200      1210      1220

    1170        1180      1190         X
  CTCTCTACAG--TCAAGGGTCTTGTTGTACAGGGACAT
  ||  | || |   |||  |||   | | ||       |
  CTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTG
       1230      1240      1250      1260      1270

2. US-09-910-186A-23' (1-1200)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score      =     73  Optimized Score      =    449  Significance =  0.58
Residue Identity   =    42%  Matches              =    527  Mismatches   =   653
Gaps               =     62  Conservative Substitutions                  =     0

                      X       10        20        30        40        50
                      TTAGTTCTGGAAGCTGTTGTTTACCTTTGCCTTCAGCTTGTCGACCTCACCG
                       ||  ||  |||  |  |   |||||    | | | | ||     |  | |
  CTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCC
   20        30        40        50        60        70        80

        60        70        80        90       100       110       120
  ACCAGGATGATGTTATGGGAGTCGATCAGGTTGATCAGCTTTGCCTTGGTGTTTCGGTCGAACTCGTTCAGC
  |      ||||   |   |  ||| | | | |    |  |   | | |||  |   ||  |  ||| || |
  AATCACCTGAT-CGACCTGTCTCGCT-ACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGA
 90       100       110       120       130       140       150

     130       140          150       160       170       180       190
  TCGTCGATGACCTTAGGCAGCATGT---TCTTGAACAGGTAGGTGACGGAGCACTCTCGGATGAACTTGTTG
  ||| | |  | |  |  ||||   |   ||| |||           || ||   || | || |||     |
  TCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATC-CTGAAGAATGCTATC
160       170       180       190       200       210        220       230

      200       210       220       230       240       250       260
  ATGTTGTTCATTGCCTCCGAGATCTTGACGTCCAGACTGTTCTTCAGGTTCTCAACCTGGCTCTTGATGTTC
   | |    |  |   | ||| | |||  |  ||    | |   || |  || | |  |   ||       ||
  GTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATC
         240       250       260       270       280       290       300

    270       280       290       300       310       320       330
  TCCTTGTCGCTTCCGGAGTACTTCTTGTACTCCAGGTCGATCTTAGCCTTGATTGCACCTGCCTGGTAGTTC
  ||  ||     |    |   | || |  ||| || |   | |  |  || | | | |  |  ||   |  |
  TCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAAC-AATTCTGGTTGGAAAGTATCTCTGAACTA
       310       320       330       340        350       360       370

  340       350             360       370       380       390       400
  AGGGAGTCGTACATCTG------GTAGGAGATGTTGTTGAACTGGGTGATGATCCTGGACAACCACGTTCCC
   ||        ||||||      | |||| |    |   | |     |    |  |   |||  ||  ||
  CGG--TGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAG
        380       390       400       410       420       430       440

      410       420       430       440       450       460       470
  ATCATCCACTCGTAGGAGTCCTTCCATCTCTTGATCCTCTGCTCCAGACAGTTGTCGATGGTCTTGATGATC
  || ||| ||   |  || | | || ||| || |||| ||    ||  |       | || ||| |||  | |
  ATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACC--ATCACCAACAATCGTC-TGAATAAC
      450       460       470       480         490       500        510

    480       490       500       510       520       530       540
  TCGTTTCGCTCCTGGACCTTACTGTAGATCACGAATGCACCCAGAGCAGGGATTGTGAACTCAGGGAATGCC
  ||      || |   | |   |    ||||    |   ||| |   |     | |  |||        | |
  TCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCT
       520       530       540       550       560       570       580

  550       560       570       580       590       600       610
  TCCAGCAGGATGGTGACACCAGTGACTGCGAATGCCTCAGTGAAGTTTCCACGACGCACAGAGTTGGAGATG
     | ||  ||| | | ||  |    |     || | |       |      |   || | | ||  |  ||
  AATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTG
     590       600       610       620       630       640       650

620       630       640       650       660       670        680       690
  TTCAGTGCGGGTCCGATGTAGGGGATGATAGCTGACACATCTGAGATCTTGTCC-AGTGTGTCCTTACGCAG
  |||      |  | ||   |       ||    |||   |  || | |  |||| | | ||   |   | |
  TTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAA
   660       670       680       690       700       710       720

          700       710       720                   730       740       750
  GATGTTGGTAGTGAAGTCCTCAACCACGTC----------GTTTGCCCA--CATCAGGAACAGACCACCTTG
  ||  |  |  ||||   |||  |  ||| |             |||  |  |   | || | || ||  |
  GACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATAC
 730       740       750       760       770       780       790       800

          760       770       780         790       800       810
  CACACCGGCATTCACCTTGTTAGCCAGGGT---AGGGAAGTAAGTGTACACCTTTGCACTGTTGTCCAGAGC
       || ||   |  | | || ||  |||   | | |  | |  |  |  | | |  ||||| |    | |
  GTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACC
          810       820       830       840       850       860       870

820        830       840       850        860       870       880
  CTCCTCGA-TTGAACGCGTGAAAGTGAAGTCCT-CCACGTTGTCACTCAGCTTCTGAGACTCTAGGTAGTAG
    | || |  ||||| | |    ||   ||  | |||  ||     |||     |  |  ||| |  |  ||
  AACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAG
       880       890       900       910       920       930       940

890           900       910       920       930       940       950
  TAGGA----GTTCAGGTAGTCCACGTTCTGGGTACGGTTGTCGTAGAAGACTTGATTCTCCCCTGGCAGGAT
   |  |    ||||         |   | |    |    ||| ||||   |    |       | | | || |
  GACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCT
     950       960       970       980       990      1000      1010

  960       970       980       990      1000            1010      1020
  CTCACTCTCACTGTCGATACTAGGGTAGAGCAGGTCTAGTTGTCCATG---CTCGGAGGTGTTCTTACTGAG
    || |    ||    |  || | |||||  || ||| ||   |  ||    ||   |  |||  || |  |
    ACCAAT---GCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTG
    1020         1030      1040      1050      1060      1070      1080

    1030       1040       1050      1060      1070      1080      1090
    GATCA-CTTGGTCTACTGACA-CGTTGTCTGGGTAGTAGATCACCTCAGTCTCCTCGTTGATGTCCTTACGC
      |||  | | | || ||| | |   |   |   ||   |||||       | |    |||      |  ||
    TCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGA-----ATCTGC
     1090      1100      1110      1120      1130      1140           1150

    1100      1110      1120      1130      1140      1150          1160
    AGGAAGATGTCAGTCTTCACGTCACTGATGTCACCGATGAATGGCAGGTCAGTGTT----CTTCACCAGCAG
    ||||  |   || |  | |||  |  | | ||| || |      ||| |||    |    ||  ||  |  |
    AGGACAA---CAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTG
           1160      1170      1180      1190      1200      1210      1220

      1170        1180      1190         X
    CTCTCTACAG--TCAAGGGTCTTGTTGTACAGGGACAT
    ||  | || |   |||  |||   | | ||       |
    CTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTG
         1230      1240      1250      1260      1270

3. US-09-910-186A-23' (1-1200)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =      28  Optimized Score  =     440  Significance = -1.15
Residue Identity  =     40%  Matches          =     539  Mismatches   =   647
Gaps              =     154  Conservative Substitutions              =     0

          X 10        20        30        40        50        60        70
    TTAGTTCTGGAAGCTGTTGTTTACCTTTGCCTTCAGCTTGTCGACCTCACCGACCAGGATGATGTTATGGA
           |||           |||  || |      ||   | |  ||| |    |      |   |  |
          ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGAC
          X       10        20        30        40        50        60

          80        90       100       110       120       130         140
    GTCGATCAGGTTGATCAGCTTTGCCTTGGTGTTTCGGTCGAACTCGTTCAGCTCGTCGATGACCTTA--GGC
      | ||| | | |||| |  | |    ||||| |   || |||   ||  |   ||  | ||| || |  | |
    AACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAA---GTATACGACGGTGTTGAACTGAATGAC
      70        80        90       100          110       120       130

         150       160       170       180       190                  200
    AGCATGTTCTTGAACAGGTAGGTGACGGAGCACTCTCGGATGAACTTGTT-----------GATGTTGTTCA
    |  |     || ||   |       | |   |||||  |||   | ||||           ||   |  ||
    AAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGAT--CCGTGTTACTCAGAATCAGAACATCATCT
      140       150       160       170         180       190       200

        210       220       230       240       250       260          270
    TTGCCTCCGAGATCTTGACGTCCAGACTGTTCTTCAGGTTCTCAACCTGGCTCTTGATGTTCTCC---TTGT
    |   |||||   || ||   | |    | | |||| || ||   | |  |   |  | |  |  |    |
    TCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCC
      210       220       230       240       250       260       270

         280       290       300       310       320       330
    CGCTTCCGGAGTACTTCTTGTACTCCAGGTCGATCTTAGCCTTGATTGCACCTGCCTGGTAGTTC-------
     |  |       ||      ||| |||     | ||       || |    |||  ||| || ||
    AGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCC
    280       290       300       310       320       330       340

     340        350       360       370       380       390       400
    -AGGGAGTCGTA-CATCTGGTAGGAGATGTTGTTGAACTGGGTGATGATCCTGGACAACCACGTTCCCATCA
      || |  |||| |||||||     |||     | ||| |   ||  |     |    |  ||    || ||
    GCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACA
  350       360       370       380       390       400       410       420

    410             420       430       440              450       460
    TCC------ACTCGTAGGAGTCCTTCCATCTCTTGATCCTC-------TGCTCCAGACAGTTGTCGATGGTC
    |||      ||   |  || | | || ||| || | || ||       |   | | |   |   | ||| |
    TCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTA
          430       440       450       460       470       480       490

     470       480       490       500       510       520       530
    TTGATGATCTCGTTTCGCTCCTGGACCTTACTGTAGATCACGAATGCACCCAGAGCAGGGATTGTGAACTCA
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        |  ||         |||||   || |   ||   | ||  || || | | ||  || |  |||
  AAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCC-GTGAAGTTATCGCTAACGGT
      500       510       520       530       540        550       560

 540        550       560       570       580         590
  GGGA-ATGCCTCCAGCAGGATGGTGACACCAGTGACTGCGAATGCCTCAG--TGAAGT-----------TTC
  |  |    | || | | ||| ||||||| |  |     | | | | || |  |||| |           |||
  GAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTC
     570       580       590       600       610       620       630

   600       610               620        630       640       650
  CACGACGCACAGAGT--------TGGAGATGTTCAGTGC-GGGTCCGATGTAGGGGATGATAGCTGACACAT
   ||  || || |  |        |   || |  | || |  | |||  | |        ||| |||| | |
  AACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGAC
   640       650       660       670       680       690       700

660       670       680       690       700       710        720       730
  CTGAGATCTTGTCCAGTGTGTCCTTACGCAGGATGTTGGTAGTGAAGTCCT-CAACCACGTCGTTTGCCCAC
   |  |   |  |||  ||       ||  || ||  |    ||  | | ||  || || |   | |   | |
  TTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATC
 710       720       730       740       750       760       770       780

         740            750       760       770       780       790
  ATCAGGAACAGA-----CCACCTTGCACACCGGCATTCACCTTGTTAGCCAGGGTAGGGAAGTAAGTGTA--
  |    ||| | |      |   |||   |    |   | | ||   |        ||     ||| |  |
  AAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATC
         790       800       810       820       830       840       850

             800       810       820       830       840       850
  ---------CACCTTTGCACTGTTGTCCAGAGCCTCCTCGATTGAACGCGTGAAAGTGAAGTCCTCCACGTT
            |||| | ||  | ||   ||  | || ||  | | |    | |   | |   | || | | |
  AACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGAT
       860       870       880       890       900       910       920

 860                                 870       880                890
  GTCA--------------------------CTCAGCTTCTGAGACTCTAGGTAGTA---------GTAGGAG
  | ||                          ||   |||||   ||   |   || |          ||
  GACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACC
     930       940       950       960       970       980       990

    900       910       920       930       940       950        960
  TTCAGGTAGTCCACGTTCTGGGTACGGTTGTCGTAGAAGACTTGATTCTCCCCTGGC-AGGATCTCACTCTC
  | || ||| | || |      | |     |   |    | ||    ||||   |  | | || |||     |
  TACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAAC
  1000      1010      1020      1030      1040      1050      1060

   970       980       990      1000        1010      1020      1030
  ACTGTCGATACTAGGGTAGAGCAGGTCTAGTTGTCC--ATGCTCGGAGGTGTTCTTACTGAGGATCACTTGG
  ||  || | |  |  | | |  | |   ||  | ||   |  |   || || | ||   ||
  ACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAA
1070      1080      1090      1100      1110      1120      1130      1140

  1040      1050      1060      1070      1080      1090      1100
  TCTACTGACACGTTGTCTGGGTAGTAGATCACCTCAGTCTCCTCGTTGATGTCCTTACGCAGGAAGATGTCA
  |||||||  |||   || |  |  | | |  || | || ||  |     ||   |       |||||   ||
  TCTACTG--ACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCGAAGAATACA
          1150      1160      1170      1180      1190      1200      1210

        1110      1120      1130                            1140      1150
  --------GTCTTCACGTCACTGATGTCACCGATGAATG----------------------GCAGGTCAGTG
           ||| ||  ||      ||  | || | | |                       | |  |  ||
  AAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTT
        1220      1230      1240      1250      1260      1270      1280

        1160      1170      1180      1190      1200
  TTCTTCACCAGCAGCTCTCTACAGTCAAGGGTCTTGTTGTACAGGGACAT
      |   |||    || | | || | | |||      | | ||  || |
  GCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCTAGAGTCGAGGCCTGCAG
      1290      1300      1310      1320      1330 X    1340      1350
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> O <
O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-24.res made by bobryen on Thu 7 Nov 102 14:36:15-PST.


Query sequence being compared:US-09-910-186A-24 (1-399)
Number of sequences searched:                      3
Number of scores above cutoff:                     3

      Results of the initial comparison of US-09-910-186A-24 (1-399) with:
        File : US08123975A.pep
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -     *
N     -
C     -
E     -                                                              *
S    0---------------------------------------------------------------------
      |      | |    |      |      |      |      |      |      |      |
SCORE 0     21 |   41     62     83    103    124    145    165    186
STDEV          0                                1


                          PARAMETERS

Similarity matrix       PAM-150    K-tuple                  1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty         20
Gap penalty               5.00     Window size            399
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                         SEARCH STATISTICS

Scores:                 Mean      Median     Standard Deviation
                        74        19           96.71

Times:                  CPU                  Total Elapsed
                    00:00:00.00              00:00:00.00

Number of residues:                    1704
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name     Description                      Length Score Score  Sig. Frame
----------------------------------------------------------------------------------
                   ****  1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U    850   186   263   1.16    0
                   ****  0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U    415    19   177  -0.57    0
  3. US-08-123-975A-5 Sequence 5, Application U    439    18   175  -0.58    0


1. US-09-910-186A-24 (1-399)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =     186  Optimized Score   =     263  Significance =  1.16
Residue Identity  =     34%  Matches           =     136  Mismatches   =   223
Gaps              =       1  Conservative Substitutions                =    33

            10        20        30        40        50        60        70
    MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
                  | | || ||:|      |      |   |   |      :   ||         |
           APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSE
           X       10        20        30        40        50        60

          80        90       100       110       120       130       140
    YPSIDSESEILPGENQVFYDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFP-TLA
          :  :           :    |    : || ||     : |   | | ::||  | ||| :|
    NTESLTDFNVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYI
       70        80        90       100       110       120       130

        150       160       170       180       190       200       210
    NKVNAGVQGGLFLMWANDVVEDFTTNILRKDTLDKISDVSAIIPYIGPALNISNSVRRGNFTEAFAVTGVTI
       |  | :|||  |   :| ||     :  |:|||:|:| |:|||| |||: |   :|||  || : |  |
    KTANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
    140       150       160       170       180       190       200

      220       230       240       250       260       270       280
    LLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWLSRIITQFNNISYQMYDS
    |||  ||  ||  |||   | :  :| ||||||| |  |  :| | |    : ||| : |||  |   || :
    LLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
  210       220       230       240       250       260       270       280

    290       300       310       320       330       340       350
    LNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVIDE
    ||||| |    |   |  ||  :| ||          |   |  |  ||| ||  ||| || | | |  ::
    LNYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
          290       300       310       320       330       340       350

  360       370       380       390        X
    LNEFDRNTKAKLINLIDSHNIILVGEVDKLKAKVNNSFQN
    | :||   |  | | ||     |:|  :  |:|||
    LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFN
        360       370       380       390  X    400       410


2. US-09-910-186A-24 (1-399)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =      19  Optimized Score   =     177  Significance = -0.57
Residue Identity  =      7%  Matches           =      30  Mismatches   =   342
Gaps              =       6  Conservative Substitutions                =    22

     X      10        20        30        40        50        60        70
    MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
           |                    :                ::     :          ||
     RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKY
     X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    YPSIDSESEILPGENQVFYDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFPTLAN
    : ||    |                  |      |           | :   |            :     |
    FNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMI--NISDYINRWIFVTITNN
           80        90        100       110       120         130       140
       150       160       170       180       190         200       210
    KVNAGVQGGLFLMWANDVVEDFTTNILRKDTLDKISDVSAIIPYIGPAL--NISNSVRRGNFTEAFAVTGVT
    : |         :     :            : |         ||                  : :
    RLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNS
          150       160       170       180       190       200       210

       220       230       240       250       260       270       280
    ILLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWLSRIITQFNNISYQMYD
      |  |          :           :   : |         |      | |        :    :
    GILKDFWGDYLQYDKPYYMLNLYDPNKYV--DVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKK
        220       230       240         250       260       270       280

     290       300       310       320       330       340       350
    SLNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVID
            |    |  |       ||   :          :  :     :
    YASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCK
        290       300       310       320       330       340       350

   360       370       380       390        X
    ELNEFDRNTKAKLINLIDSHNIILVGEVDKLKAKVNNSFQN
                 |      ||            :  |
    MNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
      360       370       380       390     X 400       410


3. US-09-910-186A-24 (1-399)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     18  Optimized Score  =     175  Significance = -0.58
Residue Identity =    10%  Matches          =      45  Mismatches   =   325
Gaps             =     29  Conservative Substitutions              =    26

    X       10        20        30        40        50        60        70
    MSLYNKTLDCRELLVKNTDLPFIGDISDVKTDIFLRKDINEETEVIYYPDNVSVDQVILSKNTSEHGQLDLL
       ||        |          | |     :     :       :     :   :    |         |
    FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFL
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    YPSIDSESEILPGENQVFYDNRTQNVDYLNSYYYLESQKLSDNVEDFTFTRSIEEALDNSAKVYTYFPTLAN
      |:     |    |              |        | |        |           |   :
    DFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLI---DINGKTKSVFFEYNIRE
          80        90       100       110       120         130       140

       150       160       170       180       190       200
    KVNAGVQGGLFLMWANDVVEDFTTNILRKDTLDKISDVSAIIPYIGPALNISNSVRRGNFT-----------
     :   :    |    |           : :    | |:  :|            : |  |
    DISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTE
          150       160       170       180       190       200       210

             210       220       230       240       250       260       270
    -------EAFAVTGVTILLEAFPEFTIPALGAFVIYSKVQERNEIIKTIDNCLEQRIKRWKDSYEWMMGTWL
           | : :      |  |          :  :        |    |        | |
    LSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYR
        220       230       240       250       260       270       280

                280       290       300       310       320       330
    S-----RIITQFNNISYQMYDSLNYQAGAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNIN
          : |      |    |        |                   |   | |  :      |  | |
    DLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQ
      290       300       310       320       330       340       350

    340       350       360       370          380       390        X
    KFIRECSVTYLFKNMLPKVIDELNEFDRNTKAKLIN---LIDSHNIILVGEVDKLKAKVNNSFQN
        :   ||    :  |  :   |       :        :            ||      :
    IKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQ
    360       370       380       390       400       410       420 X

    FIPKDEGWTE
  430
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25.res made by bobryen on Thu 7 Nov 102 14:48:41-PST.


Query sequence being compared:US-09-910-186A-25 (1-1161)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

      Results of the initial comparison of US-09-910-186A-25 (1-1161) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                         *
N     -
C     -
E     -                                                  *
S    0------------------------------------------------------------------
       |    ||    ||    |  |   |  |  |   |   ||     ||    |  |  |
SCORE 0    18    37|   55  |  73  | 92    110    128|   147  | 165
STDEV      -5     -4       -3      -2      -1       0        1

                        PARAMETERS

Similarity matrix      Unitary    K-tuple                 4
Mismatch penalty             1    Joining penalty        30
Gap penalty               5.00    Window size           500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                        SEARCH STATISTICS

Scores:                  Mean       Median     Standard Deviation
                         139        127          22.52

Times:                   CPU                     Total Elapsed
                     00:00:00.00                 00:00:00.00

Number of residues:                4027
Number of sequences searched:         3
Number of scores above cutoff:        3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                         Init. Opt.
Sequence Name      Description                   Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
   1. US-08-123-975A-6 Sequence 6, Application U   1351   165   453   1.15   0
                  ****  0 standard deviation from mean ****
   2. US-08-123-975A-4 Sequence 4, Application U   1338   126   443  -0.58   0
   3. US-08-123-975A-1 Sequence 1, Application U   1338   126   443  -0.58   0


1. US-09-910-186A-25 (1-1161)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    165  Optimized Score  =     453  Significance =  1.15
Residue Identity  =    43%  Matches          =     528  Mismatches   =   610
Gaps              =     88  Conservative Substitutions               =     0

     X       10        20        30        40        50        60        70
     ATGGCCAACTCCCGTGACGACTCCACCTGCATCAAGGTCAAGAACAACAGACTGCCATACGTTGCCGACAA-
     |||||   |  |    || | |||     | | ||    |  | |   |  ||||  |||   | | ||||
     ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAAT
     X       10        20        30        40        50        60        70

            80           90       100       110       120         130
     GGACTCCATCTCCCAGG---AGATCTTCGAGAACAAGATCATCACCGACGAGACC--AACGTTCAAAACTAC
         || ||||  | ||    | |  |  ||   |||   |  || |    || |  || |   | ||| |
     CTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAG
           80        90       100       110       120       130       140

    140       150       160          170       180       190       200
     TCCGACAAGTTCTCTTTGGACGAGTC---CATCCTGGACGGTCAGGTCCCAATCAACCCAGAGATCGTCGAC
     | | |   |  |||||  |   | ||    ||||  |    ||||   |  | || |      | |  ||
     TTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTA
        150       160       170       180       190       200       210

     210       220       230       240       250       260       270
     CCACTGTTGCCAAACGTCAACATGGAGCCATTGAACTTGCCAGGTGAGGAGATCGTCTTCTACGACGACATC
        |||         ||   | |   |      | |  |  |    || |   ||   || |  |  |||||
     TTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAATTACATC
      220       230       240       250       260       270       280

   280       290       300       310       320       330       340       350
     ACCAAGTACGTCGACTACTTGAACTCCTACTACTACTTGGAGTCTCAAAAGTTGTCTAACAACGTCGAGAAC
       |||  |   |  |  | | |||| |    |  |         |   ||| | || | |  ||   |
     CACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGT
    290       300       310       320       330       340       350       360

           360       370       380       390       400          410       420
     ATCACCTTGACCACCTCCGTCGAGGAGGCCTTGGGTTACTCTAACAAGATC---TACACCTTCCTGCCATCC
     |||| || |||      ||      | |    |    | |||       ||   |||| | |||    |  |
     ATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGTGAAGAC
            370       380       390       400       410       420       430

           430       440       450       460       470       480       490
     TTGGCTGAGAAGGTTAACAAGGGTGTTCAAGCTGGTTTGTTCCTGAACTGGGCCAACGAGGTCGTCGAGGAC
      |  ||||  |  | ||             ||||| || ||| | | |    ||||  |  |   | | |
     ATCTCTGAATACATCAA-----------TCGCTGG-TTCTTCGTTACCATCACCAATAACCTGAACAATG--
          440                  450        460       470       480       490

         500       510       520       530       540       550       560
     TTCACCACCAACATCATGAAGAAGGACACCCTGGACAAGATCTCCGACGTCTCCGTCATCATCCCATACATC
            | || |||   |  || |  |  |||||    |   ||||| ||   | ||||     |   |||
     -------CTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATC
                       500       510       520       530       540       550

       570       580        590       600       610       620       630
     GGTCCAGCCTTGAACATC-GGTAACTCCGCCCTGAGAGGTAACTTCAACCAGGCCTTCGCCACCGCCGGTGT
     | |   |     | ||||    ||||   |  ||| |   | | | | ||||  | ||   |         |
     GCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGT-ACCCAGTTCATCTGGATGAAATACTT
       560       570       580       590       600        610       620

      640       650       660       670       680       690       700
     CGCCTTCCTGCTGGAGGGTTTCCCAGAGTTCACCATCCCAGCCCTGGGTGTCTTCACCTTCTACTCCTCCAT
   | || || |       |   |  |  ||| ||  |||  ||  | |       ||   |  ||||||
   CTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATA
    630       640       650       660       670       680       690

   710                720       730       740       750       760       770
   CCAGGA---------GAGAGAGAAGATCATCAAGACCATCGAGAACTGCTTGGAGCAGAGAGTCAAGAGATG
   || | |         | |  |   | | ||  | | ||  ||  |||   ||    |    |  || |
   CCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAA
  700       710       720       730       740       750       760       770

          780       790         800         810       820       830
   GAAGGACTCCTACCAGTGGATGG--TTTCCAACTG--GCTGTCCAGAATCACCACCCAATTCAACCACATC-
        ||  | | | |  ||  |  | |||   ||  |   ||| || ||    || ||| |||||| | |
   CTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTC-GTTCCAAATACAACCAGAACT
          780       790       800       810       820        830       840

     840       850       860       870       880         890           900
   --AACTACCAGATGTACGACTCCCTGTCCTACCAGGCCGACGCCATCA--AGGCCAAGATCGACCT----GG
     || |||   |  |||  |  ||||| |  |   |   |   |||||   | |  | ||| | ||    |
   CTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGT
         850       860       870       880       890       900       910

         910       920       930       940       950       960       970
   AGTACAAGAAGTACTCCGGTTCCGACAAGGAGAACATCAAGTCCCAGGTCGAGAACCTGAAGAACTCCTTGG
       |||  |  ||  ||      |  | ||  ||||| |     |  ||   ||||||||  |    | |
   CCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGC
       920       930       940       950       960       970       980

       980       990          1000      1010      1020      1030
   ACGTCAAGATCTCCGAG----GCCATGAACAACATCAACAAGTTCATCCGTGAGTGTTCCGT-----CACCT
     ||  | | || | ||     | |  || || |  || |  ||   | |     | ||  |     |  |
   GTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACG
     990      1000      1010      1020      1030      1040      1050

   1040      1050      1060      1070            1080      1090      1100
   ACCTGTTCAAGAACATGCTGCCAAAGGTCATCGACGAGCTG------AACAAGTTCGACCTGAGAACCAAG-
   | || | ||| | ||| | |   || |    |||||| | |       ||   | | | |||     ||||
   AACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGA
  1060      1070      1080      1090      1100      1110      1120

                      1110      1120      1130      1140      1150
   --------------ACCGAGCTGATCAACCTGATCGACTCCCACAACATCATCCTGGTTGGTGAGGTTGACT
                 || ||    |||   |||||||    ||||    ||  |     ||||   ||   |
   AAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTATTCG
1130      1140      1150      1160      1170      1180      1190      1200

1160
   AA
   ||
   AAGAATACAAAGACTACTTCTG
    X   1210      1220

2. US-09-910-186A-25 (1-1161)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    126  Optimized Score =     443  Significance = -0.58
Residue Identity =     41%  Matches         =     546  Mismatches   =   600
Gaps              =    159  Conservative Substitutions               =     0

                       X        10        20        30        40        50
                       ATGGCCAACTCCCGTGACGACTCCACCTGCATCAAGGTCAAGAACAACAGAC
                        || | | || |  |||  ||  ||    |||||   |||| | |  ||  |
   CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCA---TCAATACCTCCATCC
           10        20        30        40        50           60

          60          70        80        90       100       110
   TG-CCATACGTTGCCGA--CAAGGACTCCATCTCCCAGGAGATCTTCGAGAACAAGATCATCACCG------
   ||  | | || | |  |  |||  ||   |||  || |     || ||    ||| |||| || ||
   TGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTA
  70        80        90       100       110       120       130       140

              120       130       140       150       160       170
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   ---------ACGAGACCAACGTTCAAAACTACTCCGACAAGTTCTCTTTGGACGAGTCCATCCTGGACGGTC
             |||  | | ||   | ||  |   | |   ||||  | ||||    ||||   | || | |
   AAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTT-
         150       160       170       180       190       200       210

  180       190       200       210       220       230       240       250
   AGGTCCCAATCAACCCAGAGATCGTCGACCCACTGTTGCCAAACGTCAACATGGAGCCATTGAACTTGCCAG
      |||  |  ||  |     |   | || |  |||    |||| ||  ||      | ||     | |
   --ATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCA---CCTCCTTCTGGATCCGTA
          220       230       240       250       260          270

          260       270       280       290       300       310       320
   GTGAGGAGATCGTCTTCTACGACGACATCACCAAGTACGTCGACTACTTGAACTCCTACTACTACTTGGAGT
       | |   | ||  || |  |    | | |||  |   |  |  | | |||| |    |  ||
   TCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTG
 280       290       300       310       320       330       340       350

        330       340       350       360           370
   CTCAAAAGTTGTCTAACAACGTCGAGAACATCACCTTGAC----CACCTCCGTCGAG--------------G
    |   ||  | |||   |||  ||   | |||| || |||    ||   |  ||  |              |
   GTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
         360       370       380       390       400       410       420

    380       390       400            410              420       430
   AGGCCTTGGGTTACTCTAACAAGATCTACACCT-----TCCTGCCATC-------CTTGGCTGAGAAGGTTA
     |  ||    |||||| | | |||| ||| ||     | |  | |||       ||| | |   |     |
   TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCA
       430       440       450       460       470       480       490

    440       450       460       470       480       490       500
   ACAAGGGTGTTCAAGCTGGTTTGTTCCTGAACTGGGCCAACGAGGTCGTCGAGGACTTCACCACCAACATCA
   ||||  || |  |           ||   | |   | |     | ||| | || |    | | ||||  |
   ACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGG
     500       510       520       530       540       550       560

  510       520       530           540       550       560       570
   TGAAGAAGGACACCCTGGACAAGATC----TCCGACGTCTCCGTCATCATCCCATACATCGGTCCAGC----
     || |   || |     | || |||    ||  ||    | ||  || |  ||  || || | || |
   GTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGA
   570       580       590       600       610       620       630

               580       590       600       610        620       630
   -------CTTGAACATCGGTAACTCCGCCCTGAGAGGTAACTTCAAC-CAGGCCTTCGCCACCGCCGGT---
          ||| ||  |     ||   |  ||||  |  ||    | |  || |||   | ||  || ||
   TCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCA
 640       650       660       670       680       690       700       710

             640           650                    660       670       680
   ------GTCGCCT----TCCTGCTGGAGGGTTTCCC-------------AGAGTTCACCATCCCAGCCCTGG
         ||  |||      || |||| | |  | ||             |  || |  ||| |     |||
   ATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGT
         720       730       740       750       760       770       780

        690           700       710       720       730       740       750
   GTGTCTTCACCTTCTAC----TCCTCCATCCAGGAGAGAGAGAAGATCATCAAGACCATCGAGAACTGCTTG
     |     | |   |||     | || |    | || |     | | |     |||    ||  | || ||
   ACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTG
       790       800       810       820       830       840       850

               760       770       780       790       800
   GAGC-----AGAGAGTCAAGAGATGGAAGGACTCCTACCAGTGGATGGTTTCCAACTGGCT-----------
   |  |      ||    ||| |  |    | |||| | || ||     | | |||| |   |
   GTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAAT
     860       870       880       890       900       910       920

        810       820       830       840       850       860       870
   ----GTCCAGAATCACCACCCAATTCAACCACATCAACTACCAGATGTACGACTCCCTGTCCTACCAGGCCG
       ||| | | ||    | |  ||   | || |||  | |   | |||  |    |        ||  |
   ACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACA
   930       940       950       960       970       980       990

                  880       890       900       910       920       930
   A------------CGCCATCAAGGCCAAGATCGACCTGGAGTACAAGAAGTACTCCGGTTCCGACAAGGAGA
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    |             || | ||| ||       |     |   | ||||  |  || | |   || |    |
    AAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGG
 1000      1010      1020      1030      1040      1050      1060      1070

             940       950             960       970       980       990
    AC------ATCAAGTCCCAGGTCG------AGAACCTGAAGAACTCCTTGGACGTCAAGATCTCCGAGGCCA
    ||      |    ||| ||||| |       |||    ||||||  |  ||   |||  | |         |
    ACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAA
         1080      1090      1100      1110      1120      1130      1140

         1000      1010      1020      1030         1040      1050      1060
    TGAA---CAACATCAACAAGTTCATCCGTGAGTGTTCCGTC---ACCTACCTGTTCAAGAACATGCTGCCAA
    ||||     |   ||||||    | |  |    ||| | ||     | ||| |||||| || ||      |
    TGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAAC
       1150      1160      1170      1180      1190      1200      1210

          1070      1080      1090      1100      1110      1120      1130
    AGGTCATCGACGAGCTGAACAAGTTCGACCTGAGAACCAAGACCGAGCTGATCAACCTGATCGACTCCCACA
     |||      | |   | ||||      | | ||| | ||       ||   ||  |||     |||
    TGGTTGCTTCCAACTGGTACAA-----TCGTCAGATCGAACGTTCCTCT-CGCACTCTGGGTTGCTCTTGGG
     1220      1230           1240      1250       1260      1270      1280

        1140      1150          X
    ACATCATCCTGGTTGGTGAGGTTGACTAA
    |  |||||| ||||| ||| | |
    AGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGG
         1290      1300      1310      1320      1330


3. US-09-910-186A-25 (1-1161)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =    126  Optimized Score   =    443  Significance = -0.58
Residue Identity =    41%  Matches           =    546  Mismatches   =   600
Gaps             =    159  Conservative Substitutions                =     0

                        X       10        20        30        40        50
                        ATGGCCAACTCCCGTGACGACTCCACCTGCATCAAGGTCAAGAACAACAGAC
                         || | | || |  |||  ||  ||    |||||   |||| | |  ||  |
    CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCA---TCAATACCTCCATCC
            10        20        30        40        50           60

           60          70        80        90       100       110
    TG-CCATACGTTGCCGA--CAAGGACTCCATCTCCCAGGAGATCTTCGAGAACAAGATCATCACCG------
    ||  | | || | |  |  |||  ||   |||  || |     || ||    ||| |||| || ||
    TGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTA
   70        80        90       100       110       120       130       140

               120       130       140       150       160       170
    ---------ACGAGACCAACGTTCAAAACTACTCCGACAAGTTCTCTTTGGACGAGTCCATCCTGGACGGTC
              |||  | | ||   | ||  |   | |   ||||  | ||||    ||||   | || | |
    AAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTT-
          150       160       170       180       190       200       210

   180       190       200       210       220       230       240       250
    AGGTCCCAATCAACCCAGAGATCGTCGACCCACTGTTGCCAAACGTCAACATGGAGCCATTGAACTTGCCAG
       |||  |  ||  |     |   | || |  |||    |||| ||  ||      | ||     | |
    --ATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCA---CCTCCTTCTGGATCCGTA
           220       230       240       250       260          270

           260       270       280       290       300       310       320
    GTGAGGAGATCGTCTTCTACGACGACATCACCAAGTACGTCGACTACTTGAACTCCTACTACTACTTGGAGT
        | |   | ||  || |  |    | | |||  |   |  |  | | |||| |    |  ||
    TCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTG
  280       290       300       310       320       330       340       350

         330       340       350       360           370
    CTCAAAAGTTGTCTAACAACGTCGAGAACATCACCTTGAC----CACCTCCGTCGAG--------------G
     |   ||  | |||   |||  ||   | |||| || |||    ||   |  ||  |              |
    GTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
          360       370       380       390       400       410       420

     380       390       400            410              420       430
```

```
    AGGCCTTGGGTTACTCTAACAAGATCTACACCT-----TCCTGCCATC-------CTTGGCTGAGAAGGTTA
      |  ||    |||||| | | |||| ||| ||     | |  | |||       ||| | |   |     |
    TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCA
        430       440       450       460       470       480       490

     440       450       460       470       480       490       500
    ACAAGGGTGTTCAAGCTGGTTTGTTCCTGAACTGGGCCAACGAGGTCGTCGAGGACTTCACCACCAACATCA
    ||||  || |  |           ||   | |   | |     | ||| | || |    | | ||||  |
    ACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGG
      500       510       520       530       540       550       560

   510       520       530           540       550       560       570
    TGAAGAAGGACACCCTGGACAAGATC----TCCGACGTCTCCGTCATCATCCCATACATCGGTCCAGC----
      || |   || |     | || |||    ||  ||    | ||  || |  ||  || || | || |
    GTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGGA
    570       580       590       600       610       620       630

                580       590       600       610        620       630
    -------CTTGAACATCGGTAACTCCGCCCTGAGAGGTAACTTCAAC-CAGGCCTTCGCCACCGCCGGT---
           ||| ||  |     ||   |  ||||  |  ||    | |  || |||   | ||  || ||
    TCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCA
  640       650       660       670       680       690       700       710

              640           650                    660       670       680
    ------GTCGCCT----TCCTGCTGGAGGGTTTCCC-------------AGAGTTCACCATCCCAGCCCTGG
          ||  |||      || |||| | |  | ||             |  || |  ||| |     |||
    ATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGT
          720       730       740       750       760       770       780

         690           700       710       720       730       740       750
    GTGTCTTCACCTTCTAC----TCCTCCATCCAGGAGAGAGAGAAGATCATCAAGACCATCGAGAACTGCTTG
      |     | |   |||     | || |    | ||  |     | | |     |||    ||  | || ||
    ACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTG
        790       800       810       820       830       840       850

                760       770       780       790       800
    GAGC-----AGAGAGTCAAGAGATGGAAGGACTCCTACCAGTGGATGGTTTCCAACTGGCT-----------
    |  |      ||    ||| |  |    | |||| | || ||     | | |||| |   |
    GTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAAT
      860       870       880       890       900       910       920

         810       820       830       840       850       860       870
    ----GTCCAGAATCACCACCCAATTCAACCACATCAACTACCAGATGTACGACTCCCTGTCCTACCAGGCCG
        |||  | | ||    | |  ||   | || |||  | |   | |||  |    |        ||  |
    ACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACA
    930       940       950       960       970       980       990

                   880       890       900       910       920       930
    A------------CGCCATCAAGGCCAAGATCGACCTGGAGTACAAGAAGTACTCCGGTTCCGACAAGGAGA
    |             || | ||| ||       |     |   | ||||  |  || | |   || |    |
    AAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGG
 1000      1010      1020      1030      1040      1050      1060      1070

             940       950             960       970       980       990
    AC------ATCAAGTCCCAGGTCG------AGAACCTGAAGAACTCCTTGGACGTCAAGATCTCCGAGGCCA
    ||      |    ||| ||||| |       |||    ||||||  |  ||   |||  | |         |
    ACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAA
         1080      1090      1100      1110      1120      1130      1140

         1000      1010      1020      1030         1040      1050      1060
    TGAA---CAACATCAACAAGTTCATCCGTGAGTGTTCCGTC---ACCTACCTGTTCAAGAACATGCTGCCAA
    ||||     |   ||||||    | |  |    ||| | ||     | ||| |||||| || ||      |
    TGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAAC
       1150      1160      1170      1180      1190      1200      1210

          1070      1080      1090      1100      1110      1120      1130
    AGGTCATCGACGAGCTGAACAAGTTCGACCTGAGAACCAAGACCGAGCTGATCAACCTGATCGACTCCCACA
     |||      | |   | ||||      | | ||| | ||       ||   ||  |||     |||
    TGGTTGCTTCCAACTGGTACAA-----TCGTCAGATCGAACGTTCCTCT-CGCACTCTGGGTTGCTCTTGGG
     1220      1230           1240      1250       1260      1270      1280

        1140      1150          X
    ACATCATCCTGGTTGGTGAGGTTGACTAA
```

```
|  |||||| ||||| ||| | |
AGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGG
     1290      1300      1310      1320      1330
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-25-inv.res made by bobryen on Thu 7 Nov 102 14:48:57-PST.

Query sequence being compared:US-09-910-186A-25' (1-1161)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

       Results of the initial comparison of US-09-910-186A-25' (1-1161) with:
         File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                  *
N     -
C     -
E     -                                     *
S    0-----------------------------------------------------------------
      |    ||     |  |    |     |    |  |    | |    |    |
SCORE 0    |5    10 | 15   20   26   | 31   36 |  41   46
STDEV     -4       -3        -2        -1       0


                          PARAMETERS

Similarity matrix          Unitary   K-tuple                4
Mismatch penalty                 1   Joining penalty       30
Gap penalty                   5.00   Window size          500
Gap size penalty              0.33
Cutoff score                     1
Randomization group              0

                      SEARCH STATISTICS

Scores:                    Mean      Median     Standard Deviation
                            41         33           8.08

Times:                     CPU                  Total Elapsed
                       00:00:00.00              00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
  1. US-08-123-975A-4 Sequence 4, Application U   1338    46   206   0.62   0
  2. US-08-123-975A-1 Sequence 1, Application U   1338    46   206   0.62   0
                **** 1 standard deviation below mean ****
  3. US-08-123-975A-6 Sequence 6, Application U   1351    32   246  -1.11   0

1. US-09-910-186A-25' (1-1161)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     46  Optimized Score   =    206  Significance =  0.62
Residue Identity  =    39%  Matches           =    236  Mismatches   =   336
Gaps              =     26  Conservative Substitutions               =     0

   560       570       580       590       600       610       620       630
    ACCTCTCAGGGCGGAGTTACCGATGTTCAAGGCTGGACCGATGTATGGGATGATGACGGAGACGTCGGAGAT
                        |      || |||| | | | ||| |   |   | || ||        |||
                        CTCGAGCCATGGCTCGTCTGCTGTCT---ACCTTCACTGAATACATCAAGAA
                        X       10        20           30        40

           640       650       660       670       680       690       700
    CTTGTCCAGGGTGTCCTTCTTCATGATGTTGGTGGTGAAGTCCTCGACGACCTCGTTGGCCCAGTTCAGGAA
    | |   ||     ||| || | |   ||      |  | |    | |  ||||  | | ||    ||   |
    CATCATCAATACCTCCATCCTGAACCTG-----CGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTAC
   50        60        70             80        90       100       110

         710       720       730       740       750       760       770
    CAAACCAGCTTGAACACCCTTGTTAACCTTCTCAGCCAAGGATGGCAGGAAGGTGTAGATCTTGTTAGAGTA
        |||   | |||| |  |  |||  ||  |   | |      |   |||    |||||  | |     |
    GCTTCCAAAATCAACATCGGTTCTAAAGTTAAC-TTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAA
     120       130       140        150       160       170       180

       780       790       800        810               820       830
    ACCCAAGGCCTCCTCGACGGAGGTGGTCAAGGTG-ATGTTCTCG--------ACGTTGTTAGACAACTTTTG
     |   |  | |||   |  || ||  ||  |  | ||| | |||         |  |||  || ||||| |
    TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
    190       200       210       220       230       240       250

    840       850       860       870       880       890       900
    AGACTCCAAGTAGTAGTAGGAGTTCAAGTAGTCGACGTACTTGGTGATGTCGTCGTAGAAGACGATCTCCTC
       ||||   | |            || || |  |  | | |     | |   |   ||| ||    || ||
    CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATACACCATCATC
  260       270       280       290       300         310       320

  910       920       930       940       950       960       970       980
    ACCTGGCAAGTTCAATGGCTCCATGTTGACGTTTGGCAACAGTGGGTCGACGATCTCTGGGTTGATTGGGAC
    | |||    |   |         |    | || |  |   | |  |  ||     |||||  |     ||||
    AACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGAC
  330       340       350       360       370       380       390       400

             990      1000        1010      1020      1030      1040
    ---CTGACCGTCCAGGATGGACTCG--TCCAAAGAGAACTTGTCGGAGTAGTTTTGAACGTTGGTCTCGTCG
       | |    || |  |  |  | |  | |||| |      |  |    |  | |     |   ||
    ACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGC
          410       420       430       440       450       460       470

  1050      1060      1070      1080      1090      1100      1110      1120
    GTGATGATCTTGTTCTCGAAGATCTCCTGGGAGATGGAGTCCTTGTCGGCAACGTATGGCAGTCTGTTGTTC
      |||  || |   |   |  | |    |   ||   | |||         |   | ||| ||||| |   |
    TGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGAC
        480       490       500       510       520       530       540

          1130       1140      1150          X
    TTGACCTTGAT-GCAGGTGGAGTCGTCACGGGAGTTGGCCAT
      ||    |||  |   |   |    ||     | |    ||
    CAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGA
      550       560       570       580       590       600


2. US-09-910-186A-25' (1-1161)
   US-08-123-975A-1 Sequence 1, Application US/08123975A
```

```
Initial Score    =     46  Optimized Score  =    206  Significance =  0.62
Residue Identity =    39%  Matches          =    236  Mismatches   =   336
Gaps             =     26  Conservative Substitutions               =     0

560       570       580       590      600       610       620       630
 ACCTCTCAGGGCGGAGTTACCGATGTTCAAGGCTGGACCGATGTATGGATGATGACGGAGACGTCGGAGAT
                     |      || |||| | | | ||| |   |   | || ||       |||
                     CTCGAGCCATGGCTCGTCTGCTGTCT---ACCTTCACTGAATACATCAAGAA
                     X       10        20          30        40

        640       650       660       670       680       690       700
 CTTGTCCAGGGTGTCCTTCTTCATGATGTTGGTGGTGAAGTCCTCGACGACCTCGTTGGCCCAGTTCAGGAA
 | |   ||     ||| || | |   ||      |  | |    | |  ||||  | | ||    ||   |
 CATCATCAATACCTCCATCCTGAACCTG-----CGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTAC
50        60        70             80        90       100       110

      710       720       730       740       750       760       770
 CAAACCAGCTTGAACACCCTTGTTAACCTTCTCAGCCAAGGATGGCAGGAAGGTGTAGATCTTGTTAGAGTA
     |||   | |||| |  |  |||  ||  |   | |      |   |||    |||||  | |    |
 GCTTCCAAAATCAACATCGGTTCTAAAGTTAAC-TTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAA
  120       130       140        150       160       170       180

    780       790       800        810              820       830
 ACCCAAGGCCTCCTCGACGGAGGTGGTCAAGGTG-ATGTTCTCG--------ACGTTGTTAGACAACTTTTG
  |   |  | |||   |  || ||  ||  |  | ||| | |||         |  |||  || ||||| |
 TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
 190       200       210       220       230       240       250

 840       850       860       870       880       890       900
 AGACTCCAAGTAGTAGTAGGAGTTCAAGTAGTCGACGTACTTGGTGATGTCGTCGTAGAAGACGATCTCCTC
    ||||   | |            || || |  |  | | |     | |   |   ||| ||   || ||
 CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCAT--CTCTCTGAACAATGAATACACCATCATC
260      270       280       290       300         310       320

910      920       930       940       950       960       970      980
 ACCTGGCAAGTTCAATGGCTCCATGTTGACGTTTGGCAACAGTGGGTCGACGATCTCTGGGTTGATTGGGAC
 | |||    |   |         |    | || |  |   | |  |  ||     |||||  |    ||||
 AACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGAC
330      340       350       360       370       380       390      400

          990       1000      1010      1020      1030      1040
 ---CTGACCGTCCAGGATGGACTCG--TCCAAAGAGAACTTGTCGGAGTAGTTTTGAACGTTGGTCTCGTCG
    | |    |||  |  |  | |   | |||| |      |  |    |  ||      |   ||
 ACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGC
       410       420       430       440       450       460       470

1050     1060      1070      1080      1090      1100      1110     1120
 GTGATGATCTTGTTCTCGAAGATCTCCTGGGAGATGGAGTCCTTGTCGGCAACGTATGGCAGTCTGTTGTTC
   |||  || |   |   |  | |   |   ||   | |||         |   | ||| ||||| |   |
 TGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGAC
     480       490       500       510       520       530       540

       1130      1140      1150           X
 TTGACCTTGAT-GCAGGTGGAGTCGTCACGGGAGTTGGCCAT
   ||    |||  |   |   |    ||     | |    ||
 CAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGA
   550       560       570       580       590       600

3. US-09-910-186A-25' (1-1161)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     32  Optimized Score  =    246  Significance = -1.11
Residue Identity =    40%  Matches          =    292  Mismatches   =   384
Gaps             =     51  Conservative Substitutions               =     0

                     X       10        20        30        40        50
                     TTAGTCAACCTCACCAACCAGGATGATGTTGTGGGAGTCGATCAGGTTGATC
                     | ||||Ъ|       |    ||   | | |   |   |    |   |   |
 ATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTG
        640       650       660       670       680       690       700

       60              70        80        90       100       110
 AGCTCGGTCTTGGTT------CTCAGGTCGAACTTGTTCAGCTCGTCGATGACCTTTGGCAGCATGTTCTTG
 |      ||| || |      || | ||  |||        ||    | | |    ||| | || |  ||
 AAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCT
      710       720       730       740       750       760       770

120       130       140         150       160       170       180
 AACAGGTAGGTGACGGAACACTCACGGAT---GAACTTGTTGATGTTGTTCATGGCCTCGGAGATCTTGACG
  |||   |  ||| | || |||| | | |     |  |  |||    | ||    |    ||| ||  |
 TACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAA
    780       790       800       810       820       830       840

 190       200       210       220       230       240       250
 TCCAAGGAGTTCTTCAGGTTCTCGACCTGGGACTTGATGTTCTCCTTGTCGGAACCGGAGTACTTCTTGTAC
 | ||   | | |  |    | |  | | | ||  |  || |   |||| ||    |   ||   |  |
 TACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATC-CGTCGCAAATCTAACTCTCAGTCCA-
  850       860       870       880       890       900       910

260      270      280       290       300       310       320
 TCCAGGTCGATCTTGGCCTTGATGGCGTCGGCCTGGTAGGACAGGGAGTCGTACATCTGGTA-----GTTGA
 || | |  ||  | |  | | | |  | |  | |     ||  ||| |  | || |  | |       ||
 TCAATGATGACATCGTACGTAAAGAAGACTACAT----CTACCTGGACTTCTTCAACCTGAATCAGGAATGG
  920       930       940       950          960       970      980

  330       340       350       360       370              380      390
 TGTGGTTGAATTGGGTGGTGATTCTGGACAGCCAGTTGGAAACCATCCACTGG--------TAGGAGTCCTT
  |||  |  |       ||  |||  || ||  ||  | ||| | |   ||||        |  || |||
 CGTGTATACACCTACAAGTACTTCAAGAAAG-AAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGA
    990     1000      1010       1020      1030     1040      1050

        400       410       420       430       440       450       460
 CCATCTCTTGACTCTCTGCTCCAAGCAGTTCTCGATGGTCTTGATGATCTTCTCTCTCTCCTGGATGGAGGA
 | | ||||  |    |  |   |   |    |     |    |  || || ||||  |     | ||    |
 CGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAA
  1060      1070      1080      1090      1100      1110      1120

      470       480       490       500       510       520       530
 GTAGAAGGTGAAGACACCCAGGGCTGGATGGTGAACTCTGGGAAACCCTCCAGCAGGAAGGCGACACCGGC
 |   ||| ||||||  |    | |      |||   || |      ||      | |||   |  | ||
 G--AAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGTATCGTA
  1130      1140      1150      1160      1170      1180      1190

    540       550         560       570       580       590       600
 GGTGGCGAAGGCCTGGTTGAAGT---TACCTCTCAGGGCGGAGTTACCGATGTTCAAGGCTGGACCGATGTA
    |  |||  |   |   |  |    | ||| |   |    | |  || ||| || ||   ||||    |
 TTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGC-AAACCGTACAA
1200      1210      1220      1230      1240      1250      1260

     610       620       630       640       650       660       670
 TGGGATGATGACGGAGACGTCGGAGATCTTGTCCAGGGTGTCCTTCTTCATGATGTTGGTGGTGAAGTCCTC
    ||   ||      |  | | || || |  | |             | || |  |||  || |
 CCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGA--------------AAGACGAAGGT--TGGACCGAAT
1270     1280     1290      1300                    1310        1320

   680       690       700 X      710       720
 GACGACCTCGTTGGCCCAGTTCAGGAACAAACCAGCTTGAACACCCT
     |||||    | | ||  | | |
 AGTAACCTCTAGAGTCGAGGCCTGCAG
   1330      1340      1350
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-26.res made by bobryen on Thu 7 Nov 102 14:36:40-PST.

Query sequence being compared:US-09-910-186A-26 (1-386)
Number of sequences searched:                         3
Number of scores above cutoff:                        3

     Results of the initial comparison of US-09-910-186A-26 (1-386) with:
       File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -    **                                                        *
S     0---------------------------------------------------------------------
      |      | |    |      |      |      |      |      |      |      |
SCORE 0     22 |   44     67     89    111    133    156    178    200
STDEV          0                                1

                                PARAMETERS

Similarity matrix        PAM-150      K-tuple                    1
Threshold level of sim.    16%
Mismatch penalty             1      Joining penalty             20
Gap penalty               5.00      Window size                386
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            78           17          105.38

Times:                     CPU                     Total Elapsed
                      00:00:00.00                  00:00:00.00

Number of residues:                   1704
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                    Init. Opt.
Sequence Name     Description              Length Score Score   Sig. Frame
-------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U    850   200   262   1.16   0
                  ****  0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U    415    19   170  -0.56   0
  3. US-08-123-975A-5 Sequence 5, Application U    439    16   101  -0.59   0


1. US-09-910-186A-26 (1-386)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    200  Optimized Score  =    262  Significance =  1.16
Residue Identity =     37%  Matches          =    143  Mismatches   =   208
Gaps              =      2  Conservative Substitutions               =    29

         X  10        20        30        40        50        60        70
    MANSRDDSTCIKVKNNRLPYVADKDSISQEIFENKIITDETNVQNYSDKFSLDESILDGQVPINPEIVDPLL
             || | |  | ::||| | | :   |  |   |        |   | |||       |
         APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENT
         X       10        20        30        40        50        60

          80        90       100       110       120       130        140
    PNVNMEPLNLPGEEIVFYDDITKYVDYLNSYYYLESQKLSNNVENITLTTSVEEALGYSNKIYTFLP-SLAE
              |  |         : |    : || ||     :  | || | ::|| :|||:| |
    ESLTDFNVDVPVYEKQ-PAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIK
     70        80         90       100       110       120       130

        150       160       170       180       190       200       210
    KVNKGVQAGLFLNWANEVVEDFTTNIMKKDTLDKISDVSVIIPYIGPALNIGNSALRGNFNQAFATAGVAFL
      || | ||||  |   :| ||     |  |:|||:|:| |:|||| |||:||   :|||  ||  || : |
    TANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASIL
   140       150       160       170       180       190       200       210

      220       230       240       250       260       270       280
    LEGFPEFTIPALGVFTFYSSIQEREKIIKTIENCLEQRVKRWKDSYQWMVSNWLSRITTQFNHINYQMYDSL
    ||  ||  ||  | |   | |  : ||||||:| |  |  :| | |   |: ||| : |||  |   || :|
    LEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKAL
           220       230       240       250       260       270       280

    290       300       310       320       330       340       350
    SYQADAIKAKIDLEYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKNMLPKVIDEL
     ||| |    |   |  ||  :| ||          |   |  |  ||| ||  ||| || | | |  :: |
    NYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEKL
         290       300       310       320       330       340       350

  360       370       380     X
    NKFDLRTKTELINLIDSHNIILVGEVD
      ||   |  | | ||     |:|  :
    LDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSI
       360       370       380       390       400


2. US-09-910-186A-26 (1-386)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     19  Optimized Score  =    170  Significance = -0.56
Residue Identity =     11%  Matches          =     44  Mismatches   =   314
Gaps              =      9  Conservative Substitutions               =    28

                   X       10        20        30        40        50
                   MANSRDDSTCIKVKNNRLPYVADKDSISQEIFENKIITDETNVQNYSDKFSLDESIL
                     |         :  |         |    |  | |:
    RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
            10     X   20        30        40        50        60        70

     60        70        80        90       100       110       120
    DGQVPINPEIVDPLLPNVNMEPLNLPGEEIVFYDDITKYVDYLNSYYYLESQKLSNNVENITLTTSVEEALG
          |   :   : |       |   ||:     |  :     : |      |  :      |     |
    NSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLN
          80        90       100       110       120       130       140
  130            140       150       160       170       180       190
    YSN-----KIYTFLPSLAEKVNKGVQAGLFLNWANEVVEDFTTNIMKKDTLDKISDVSVIIPYIGPALNIGN
     |      :     |        :    :|   :      :              :  :   |   :
    NSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
       150       160       170       180       190       200       210

     200       210       220       230       240          250       260
    SALRGNFNQAFATAGVAFLLEGFPEFTIPALGVFTFYSSIQEREKIIKT---IENCLEQRVKRWKDSYQWMV
        | : |         | :      :   |:  :      |  :  |       |    |     |
    KDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGN
     220       230       240       250       260       270       280

      270       280       290       300       310        320       330
    SNWLSRITTQFNHINYQMYDSLSYQADAIKAKIDLEYKKYSGSDKENIKSQVE-NLKNSLDVKISEAMNNIN
         |                     |  | ::         |  |    |    ||   :     ||
    KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQD
   290       300       310       320       330       340       350       360

     340       350       360       370       380     X
    KFIRECSVTYLFKNMLPKVIDELNKFDLRTKTELINLIDSHNIILVGEVD
        :                  | :          |  |   |  | :
    NNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
           370       380       390       400       410


3. US-09-910-186A-26 (1-386)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score     =      16  Optimized Score  =     101  Significance = -0.59
Residue Identity  =      8%  Matches          =      21  Mismatches   =   204
Gaps              =       6  Conservative Substitutions               =    17

                        X       10        20        30              40
                        MANSRDDSTCIKVKNNRLPYVADKDSISQEIFENKIITD------ETNVQNY
                        :    |    |  |           |   | :      :
    SNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYN
          180       190 X     200       210       220       230       240

      50        60        70        80        90        100       110
    SDKFSLDESILDGQVPINPEIVDPLLPNVNMEPLNLPGEEIVFYDDITKYVDYLNSYYYLESQKLSNNVENI
     : :          :    :              |             |::    |             : |
    KEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYI
        250       260       270       280       290       300       310

   120       130       140       150       160       170       180       190
    TLTTSVEEALGYSNKIYTFLPSLAEKVNKGVQAGLFLNWANEVVEDFTTNIMKKDTLDKISDVSVIIPYIGP
     |                |           :           : |           | |  : |
    YLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIG
      320       330       340       350       360       370       380

           200       210       220       230       240 X     250       260
    ALNIGNSALRGNFNQAFATAGVAFLLEGFPEFTIPALGVFTFYSSIQEREKIIKTIENCLEQRVKRWKDSYQ
          |:        :      :| |         ||    :    |
    IHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
    390       400       410       420       430        X
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-27.res made by bobryen on Thu 7 Nov 102 14:49:17-PST.


Query sequence being compared:US-09-910-186A-27 (1-1149)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-27 (1-1149) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                        *
N     -
C     -
E     -                                                               *
S    0----------------------------------------------------------------------
      |      |      | |    |   |  ||    ||  |   ||    ||  |    ||   | |
SCORE 0     11     22 |   33   | 44|    54  |  65|    76  |   87|   |98
STDEV                -9   -8  -7  -6   -5  -4   -3   -2  -1     0   1

                              PARAMETERS

Similarity matrix        Unitary      K-tuple                       4
Mismatch penalty               1      Joining penalty              30
Gap penalty                 5.00      Window size                 500
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                                SEARCH STATISTICS

Scores:                     Mean        Median        Standard Deviation
                              90            87            6.93

Times:                      CPU                       Total Elapsed
                       00:00:00.00                    00:00:00.00

Number of residues:                       4027
Number of sequences searched:                3
Number of scores above cutoff:               3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                             Init. Opt.
Sequence Name     Description                        Length Score Score  Sig. Frame
------------------------------------------------------------------------------------
                          ****  1 standard deviation above mean ****
   1. US-08-123-975A-6 Sequence 6, Application U  1351    98    463   1.15    0
                          ****  0 standard deviation from mean ****
   2. US-08-123-975A-4 Sequence 4, Application U  1338    86    408  -0.58    0
   3. US-08-123-975A-1 Sequence 1, Application U  1338    86    408  -0.58    0


1. US-09-910-186A-27 (1-1149)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    98  Optimized Score  =    463  Significance =  1.15
Residue Identity  =   43%  Matches          =    561  Mismatches   =   576
Gaps              =   144  Conservative Substitutions             =     0

                     X       10        20        30        40        50
                     ATGTCCATCTGCATCGAGATCAACAACGGTGAGCTGTTCTTCGTGGCTTCCG
                     |    ||||   | |  |    |||| |   |     |  |||     || |
 ACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTG
   20        30      X 40      50        60        70        80

       60        70        80        90       100                110
 AGAACAGTTACAACGATGACAACATCAACACTCCTAAGGAGATTGACGA---------CACCGTCACTTCTA
    || ||   || | |||      | ||  |  | |   || |||| |         ||   | || |||
 GTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTT
 90       100       110       120       130       140       150       160

   120       130       140          150       160        170       180
 ACAACAACTACGAAAACGACCTGGACCAG---GTCATCCTAAACTTCAACTCCG-AGTCCGCCCCTGGTCTG
  |   ||||   | | |    |    |||      | | | | ||||||||||| | |||    ||  ||||
 CCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTG
        170       180       190       200       210       220       230

       190       200       210       220       230       240       250
 --TCCGACGAGAAGCTGAACCTGACCATCCAGAACGACGCTTACATCCCAAAGTACGACTCCAACGGTACAT
   |||  |  ||  |  | || ||    | ||||||||| |   ||||  || |||  |  |||  | | |
 TTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGT---ATCCAGAATTACATCCACAA-TGAATAC
      240       250       260       270          280       290        300

     260       270        280          290       300       310       320
 CCGATATCGAGCAGCATGACG-TTAACGAGCTT---AACGTCTTCTTCTACTTAGACGCTCAGAAGGTGCCC
  | ||    | | |||||| |  ||||     |   ||  ||| | ||  |    ||  |   |    | |
 ACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACT
        310       320       330       340       350       360       370

       330              340       350       360       370       380
 GAGGGTGAGAACAACG-------TCAATCTCACCTCTTCAATTGACACAGCCTTGTTGGAGCAGCCTA--AG
   |   || | |||||         |||||    ||||| | |   ||| || ||  |      |  |  |
 CTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATAC
      380       390       400       410       420       430       440

    390       400       410       420       430       440       450
 ATCTACACCTTCTTCTCCTCCGAGTTCATCAACAACGTCAACAAGCCTGTGCAGGCCGCATTGTTCGTAAGC
 ||| |   ||  |||| |       ||| ||| ||| | |||||  |  |  |  |  |||     |||| |
 ATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGC--TAAAATCTACATCAACGGTAAAC
    450       460       470       480       490        500       510

  460         470       480         490       500       510       520
 TGGATTC--AGCAGGTGTTAGTAGACTTCACT---ACTGAGGCTAACCAGAAGTCCACTGTTGACAAGATCG
 |||| ||  |    |   |   |||| ||  |     |   ||||||    |   ||   |  |   |  ||
 TGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACG
    520       530       540       550       560       570       580

     530                                  540       550       560
 CTGACATC---------------------------TCCATCGTCGTCCCATACATCGGTCTGGCTCTGAACA
  |||||||                           | | ||  | ||    ||| ||  ||| ||| |  ||
 GTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCA
  590       600       610       620       630       640       650

570       580       590             600       610       620       630
 TCGGCAACGAGGCACAGAAGGGC------AACTTCAAGGATGCCCTTGAGTTGTTGGGTGCCGGTATTTTGT
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     | | ||     | |||  |       ||| | |  |       || || | ||||       |  |||
 ATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGT
660       670       680       690       700       710       720       730

   640       650       660       670       680
 TGGAGTTCGAACCCGAGCTGCTGATCCCTACCATCCTGGTCTTCACGATCAA--------------------
    |    |||  | |  || | |   ||    | |  |  ||     |||||
 ACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGG
       740       750       760       770       780       790       800

     690       700       710       720       730       740       750
 ----GTCCTTCCTGGGTTCCTCCGACAACAAGAACAAGGTCATTAAGGCCATCAACAACGCCCTGAAGGAGC
          |||||  |   ||| |  ||||  | ||    |   |   || | ||  || |||| |
 TTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCG
     810       820       830       840       850       860       870

   760            770                  780       790       800
 GTGACGAG-----AAGTGGAAGGAAGTCTA-----------TTCCTTCATCGTCTCGAACTGGATGA--CCA
 ||||  ||      |   |  | || ||||             ||  | ||    ||| ||   | ||   |
 GTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACT
   880       890       900       910       920       930       940

810       820       830       840                   850       860
 AGATCAACACCCAGTTCAACAAGCGAAAGGAG------------CAGATGTACCAGGCTCTGCAGAACCAGG
 | ||| ||    | |||  ||| |  ||  ||             | |  ||| ||    |  ||||  | |
 ACATCTACCTGGACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAG
  950       960       970       980       990       1000      1010

870             880       890       900       910       920
 TCAA------CGCCATCAAGACCATCATCGAGTCCAAGTACAACTCCTACACCCTGGAG------GAGAAGA
    |         | |     | |||   || ||| |  |   || | ||||| |  ||      ||  |
 AAGAAAAGCTTTTCCTGGCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACG
1020      1030      1040      1050      1060      1070      1080      1090

930       940       950       960       970       980       990       1000
 ACGAGCTTACCAACAAGTACGATATCAAGCAGATCGAGAACGAGCTGAACCAGAAGGTCTCCATCGCCATGA
 |||| |   | | | | |          || | || |||| ||     |    |  | |   ||||   |||
 ACGAACAGCCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGA
      1100      1110      1120      1130      1140      1150      1160

      1010      1020      1030      1040      1050      1060      1070
 ACAACATCGACAGGTTCCTGACCGAGTCCTCCATCTCCTACCTGATGAAGCTCATCAACGAGGTCAAGATCA
  |   ||| || | |||     ||| ||     | || ||   || |||   ||   || |  ||   |||
 TCGGTATCCACCGTTTC---TACGAATC--TGGTATCGTATTCGAAGAA-TACAAAGACTACTTCTGCATCT
    1170         1180        1190      1200       1210      1220

    1080      1090      1100      1110      1120      1130      1140
 ACAAGCTGCGAGAGTACGACGAGAATGTCAAGACGTACCTGCTGAACTACATCATCCAGCACGGATCCATCC
  |||   |     | | || |  ||   |||  |||||   |||||         | |       | |||||
 CCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCC
1230      1240      1250      1260      1270      1280      1290      1300

     X
 TGTAA
  | ||
 CGAAAGACGAAGGTTGGACCGAATA
     X 1310      1320


2. US-09-910-186A-27 (1-1149)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     86  Optimized Score =    408  Significance = -0.58
Residue Identity =    43%  Matches         =    478  Mismatches   =   571
Gaps             =     62  Conservative Substitutions             =     0

  60        70        80        90       100        110       120
 AGTTACAACGATGACAACATCAACACTCCTAAGGAGATTGACGAC-ACCGTCACTTCTAACAACAACTACGA
                     |   |  | |     |  ||  | | ||| |||||    ||| |||    ||
                     CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAA----GA
                     X       10        20        30        40

130       140       150       160       170       180       190       200
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 AAACGACCTGGACCAGGTCATCCTAAACTTCAACTCCGAGTCCGCCCCTGGTCTGTCCGACGAGAAGCTGAA
 | |  | |   |||    ||||||| ||| |   || ||| |   ||  |   |||  ||||  |   |   |
 ACATCATCAATACC--TCCATCCTGAACCTGCGCTACGAAT---CCAATCACCTGATCGACCTGTCTCGCTA
50        60          70        80           90       100       110

       210       220       230       240       250       260       270
 CCTGACCATCCAGAACGACGCTTACATCCCAAAGTACGACTCCAACGGTACATCCGATATCGAGCAGCATGA
 |    |||     |||  || ||  |     || | ||| | | ||  |      | ||| ||| |    |
 CGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAA
  120       130       140       150       160       170       180

     280       290       300       310       320       330          340
 CGTTAACGAGCTTAACGTCTTCTTCTACTTAGACGCTCAGAAGGTGCCCGAGGGTGAGAAC---AACGTCAA
   |  |       ||  ||    |   | |  |   |   |  ||   | |   |  | ||   ||| ||
 TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
190       200       210       220       230       240       250

      350       360       370       380       390       400       410
 TCTCACCTCTTCAATTGACACAGCCTTGTTGGAGCAGCCTAAGATCTACACCTTCTTCTCCTCCGAGTTCAT
    | |||  |  ||    |   |    |      |  | |        | |      | | ||    |||
 CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAA
260       270       280       290       300       310       320       330

    420       430       440         450       460       470       480
 CAACAACGTCAACAAGCCTGTGCAGGCCGCATTGTT--CGTAAGCTGGATTCAGCAGGTGTTAGTAGACTTC
 |  ||  |  |||||  |||    |   | ||   |    || | || | ||| | ||  |  | ||
 CTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAG-----
      340       350       360       370       380       390

    490       500       510       520       530       540       550
 ACTACTGAGGCTAACCAGAAGTCCACTGTTGACAAGATCGCTGACATCTCCATCGTCGTCCCATACATCGGT
    ||| |||  | | |  ||     |||   |||   | || | ||   || | ||      ||||||  |
 GACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAAT
400       410       420       430       440       450       460       470

     560           570       580       590             600       610
 --CTGGCTC----TGAACATCGGCAACGAGGCACAGAAGGGC------AACTTCAAGGATGCCCTTGAG-TT
   |||| ||    | | ||||  |||| |    | |||    |      | || ||   | | || |  | |
 CGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATC
        480       490       500       510       520       530       540

    620       630       640       650       660       670       680
 GTTGGGTGCCGGTATTTTGTTGGAGTTCGAACCCGAGCTGCTGATCCCTACCATCCTGGTCTTCACGATCAA
 |    |   | |   |    |   | |   | ||  ||| || |    || |||| || ||     |  |
 GACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAA----TAACATCATGTTCAAACTGGACGG
      550       560       570       580           590       600       610

 690       700       710       720       730       740       750
 GTCCTTCCTGGGTTCCTCCGACAACAAGAACAAGGTCATTAAGGCCATCAACAACGCCCTGAAGGAGCGTGA
  |          |  |  | ||| |  || |||   | | ||     || |||| |  ||||| ||    ||
 TTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGA
       620       630       640       650       660       670       680

   760       770       780       790       800       810       820
 ----CGAGAAGTGGAAGGAAGTCTATTCCTTCATCGTCTCGAACTGGATGACCAAGATCAACACC--CAGTT
       |||  || | |  |  |  | |  |  | || ||      ||   |   | | |  |||  ||||
 AATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTA
     690       700       710       720       730       740       750

   830       840       850           860       870       880         890
 CAACAAGCGAAAGGAGCAGATGTACC---AGGCTCTGCAGAACCAGGTCAACGCCATCAA---GACCATCAT
 | |||| |   |  |   | || | |   | | || | | ||  | ||  ||| || |||       |||
 CGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCG
   760       770       780       790       800       810       820

       900       910       920            930       940       950
 CGAGTCCAAGTACAACTCCTACACCCTGGAG-----GAGAAGAACGAGCTTACCAACAAGTACGATATCAAG
 ||  | || ||||  ||   |   ||  | |     |  | ||         | | ||  | ||  |  |  |
 CGGTTACATGTAC--CTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTG
 830       840       850       860       870       880       890

960       970       980       990       1000      1010       1020
 CAGATCGAGAACGAGCTGAACCAGAAGGTCTCCATCGCCATGAACAACATCGACA-GGTTCCTGACCGAGTC
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   |    |  | | |  | | |   |||   | |    |    |||||   | | |  ||||   ||   |
  TACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGAT
   900       910       920       930       940       950       960

1030      1040      1050      1060      1070      1080        1090
  CTCCATCTCCTACCTGATGAAGCTCATCAACGAGGTCAAGATCAACAAGCTGCGA--GAGTACGACGAGAAT
  |       | |   || || || | |  |   ||   || | |  |  ||| | |  |  |   | |    |
  CGTGTATACATCAATGTTGTAGTTAAGAACAAAG---AATACCGTCTGGCTACCAATGCTTCTCAGGCTGGT
 970       980       990      1000           1010      1020      1030

1100      1110      1120      1130      1140        X
  GTCAAGACGTACCTGCTGAACTACATCATCCAGCACGGATCCATCCTGTAA
  ||  | | |  | ||            |||| | |||     |  ||||
  GTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATC
 1040      1050      1060      1070      1080      1090      1100

3. US-09-910-186A-27 (1-1149)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    86  Optimized Score  =   408  Significance = -0.58
Residue Identity  =   43%  Matches          =   478  Mismatches   =   571
Gaps              =    62  Conservative Substitutions             =     0

   60        70        80        90       100        110       120
  AGTTACAACGATGACAACATCAACACTCCTAAGGAGATTGACGAC-ACCGTCACTTCTAACAACAACTACGA
                      |   |  | |     |  ||  | | ||| |||||    ||| |||    ||
                      CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAA----GA
                      X        10        20        30        40

 130       140       150       160       170       180       190       200
  AAACGACCTGGACCAGGTCATCCTAAACTTCAACTCCGAGTCCGCCCCTGGTCTGTCCGACGAGAAGCTGAA
  | |  | |   |||    |||||| ||| |   || ||| |   ||  |   |||  ||||  |   |   |
  ACATCATCAATACC--TCCATCCTGAACCTGCGCTACGAAT---CCAATCACCTGATCGACCTGTCTCGCTA
  50        60         70        80            90       100       110

         210       220       230       240       250       260       270
  CCTGACCATCCAGAACGACGCTTACATCCCAAAGTACGACTCCAACGGTACATCCGATATCGAGCAGCATGA
  |    |||     |||  || ||  |     || | |||  | | ||  |      | ||| ||| |    |
  CGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAA
    120       130       140       150       160       170       180

       280       290       300       310       320       330          340
  CGTTAACGAGCTTAACGTCTTCTTCTACTTAGACGCTCAGAAGGTGCCCGAGGGTGAGAAC---AACGTCAA
    |  |       ||  ||    |   | |  |   |   |  ||   | |   |  | ||   ||| ||
  TCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTC
  190       200       210       220       230       240       250

        350       360       370       380       390       400       410
  TCTCACCTCTTCAATTGACACAGCCTTGTTGGAGCAGCCTAAGATCTACACCTTCTTCTCCTCCGAGTTCAT
     | |||  |  ||    |   |    |      |  | |        | |      | | ||    |||
  CACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAA
260       270       280       290       300       310       320       330

      420       430       440        450       460       470       480
  CAACAACGTCAACAAGCCTGTGCAGGCCGCATTGTT--CGTAAGCTGGATTCAGCAGGTGTTAGTAGACTTC
  |  ||  |  |||||  |||    |   | ||   |    || | || | ||| | ||  |  | ||
  CTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAG-----
        340       350       360       370       380       390

      490       500       510       520       530       540       550
  ACTACTGAGGCTAACCAGAAGTCCACTGTTGACAAGATCGCTGACATCTCCATCGTCGTCCCATACATCGGT
     ||| |||  | | |  ||     |||   |||   | || | ||   || | ||      ||||||   |
  GACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAAT
 400       410       420       430       440       450       460       470

      560          570       580       590              600       610
  --CTGGCTC----TGAACATCGGCAACGAGGCACAGAAGGGC------AACTTCAAGGATGCCCTTGAG-TT
    |||| ||    | | ||||  |||| |    | |||   |      | || ||   | | || |  | |
  CGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATC
         480       490       500       510       520       530       540

     620       630       640       650       660       670       680
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  GTTGGGTGCCGGTATTTTGTTGGAGTTCGAACCCGAGCTGCTGATCCCTACCATCCTGGTCTTCACGATCAA
  |    |   | |   |    |   | |   | ||  ||| || |    || |||| || ||     |  |
  GACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAA----TAACATCATGTTCAAACTGGACGG
       550       560       570       580           590       600       610

  690       700       710       720       730       740       750
  GTCCTTCCTGGGTTCCTCCGACAACAAGAACAAGGTCATTAAGGCCATCAACAACGCCCTGAAGGAGCGTGA
   |          |  |  | ||| |  || |||   | | ||     || |||| |  ||||| ||    ||
  TTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGA
         620       630       640       650       660       670       680

     760       770       780       790       800       810         820
  ----CGAGAAGTGGAAGGAAGTCTATTCCTTCATCGTCTCGAACTGGATGACCAAGATCAACACC--CAGTT
        |||  || | |  |  |  | |  |  | || ||      ||   |   | | |  |||  ||||
  AATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTA
     690       700       710       720       730       740       750

     830       840       850         860       870       880           890
  CAACAAGCGAAAGGAGCAGATGTACC---AGGCTCTGCAGAACCAGGTCAACGCCATCAA---GACCATCAT
  | |||| |   |  |   | || | |   | | || | | ||  | ||  ||| || |||       |||
  CGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCG
     760       770       780       790       800       810       820

         900       910       920            930       940       950
  CGAGTCCAAGTACAACTCCTACACCCTGGAG-----GAGAAGAACGAGCTTACCAACAAGTACGATATCAAG
  ||  | || ||||  ||   |   ||  | |     |  | ||        | | ||  | ||  |  |  |
  CGGTTACATGTAC--CTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTG
   830       840         850       860       870       880       890

960         970       980       990      1000      1010      1020
  CAGATCGAGAACGAGCTGAACCAGAAGGTCTCCATCGCCATGAACAACATCGACA-GGTTCCTGACCGAGTC
   |    |  | | |  | | |   |||   | |    |    |||||   | | |  ||||   ||   |
  TACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGAT
   900       910       920       930       940       950       960

1030      1040      1050      1060      1070      1080        1090
  CTCCATCTCCTACCTGATGAAGCTCATCAACGAGGTCAAGATCAACAAGCTGCGA--GAGTACGACGAGAAT
  |       | |   || || || | |  |   ||   || | |  |  ||| | |  |  |   | |    |
  CGTGTATACATCAATGTTGTAGTTAAGAACAAAG---AATACCGTCTGGCTACCAATGCTTCTCAGGCTGGT
 970       980       990      1000           1010      1020      1030

1100      1110      1120      1130      1140        X
  GTCAAGACGTACCTGCTGAACTACATCATCCAGCACGGATCCATCCTGTAA
  ||  | | |  | ||            |||| | |||     |  ||||
  GTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATC
 1040      1050      1060      1070      1080      1090      1100
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-27-inv.res made by bobryen on Thu 7 Nov 102 14:49:34-PST.


Query sequence being compared:US-09-910-186A-27' (1-1149)
Number of sequences searched:                  3
Number of scores above cutoff:                 3

     Results of the initial comparison of US-09-910-186A-27' (1-1149) with:
       File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                           *
N     -
C     -
E     -                                                              *
S    0----------------------------------------------------------------------
       |     |     |     |     |    || |   || |   |    |  ||   || |
SCORE  0     4     9     13    18   22 |   27 |   31   | 36|   ||40
STDEV                              -9 -8  -7 -5   -4  -2  -1    1

                        PARAMETERS

Similarity matrix      Unitary    K-tuple               4
Mismatch penalty             1    Joining penalty      30
Gap penalty               5.00    Window size         500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                      SEARCH STATISTICS

Scores:             Mean      Median     Standard Deviation
                      38         38           1.73

Times:               CPU                 Total Elapsed
                00:00:00.00              00:00:00.00

Number of residues:               4027
Number of sequences searched:        3
Number of scores above cutoff:       3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                      Init. Opt.
Sequence Name     Description                 Length Score Score  Sig. Frame
----------------------------------------------------------------------------
                       ****  1 standard deviation above mean ****
  1. US-08-123-975A-6 Sequence 6, Application U   1351    40   359   1.15   0
                       ****  0 standard deviation from mean ****
  2. US-08-123-975A-4 Sequence 4, Application U   1338    37   400  -0.58   0
  3. US-08-123-975A-1 Sequence 1, Application U   1338    37   400  -0.58   0


1. US-09-910-186A-27' (1-1149)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    40  Optimized Score  =    359  Significance =  1.15
Residue Identity  =   40%  Matches          =    416  Mismatches   =   569
Gaps              =    54  Conservative Substitutions              =     0

  120       130       140       150       160       170       180       190
   GAGGACTCGGTCAGGAACCTGTCGATGTTGTTCATGGCGATGGAGACCTTCTGGTTCAGCTCGTTCTCGATC
                        | | | |     |   | ||   ||  | |||    |  || | ||  | |
                       ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                       X       10        20        30        40        50

          200       210       220       230       240       250       260
   TGCTTGATATCGTACTTGTTGGTAAGCTCGTTCTTCTCCTCCAGGGTGTAGGAGTTGTACTTGGACTCGATG
   ||| | |   |  |        |  | ||| |||        | ||||    ||||| | |      || ||
   TGCGTTA---CAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTG
            60        70        80        90       100       110       120

        270       280       290       300       310       320       330
   ATGGTCTTGATGGCGTTGACCTGGTTCTGCAGAGCCTGGTACATCTGCTCCTTTCGCTTGTTGAACTGGGTG
    ||  ||  ||| |    ||| | |    | || |||  | |     |||      |    | |    |
   TTGAACTGAATGACAAGAACCAGTTCAAACTGA-CCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAAT
         130       140       150       160       170       180       190

      340       350       360       370       380       390       400
   TTGATCTTGGTCATCCAGTTCGAGACGATGAAGGAATAGACTTCCTTCCACTTCTCGTCACGCTCCTTCAGG
     || | |  || || | | ||      || |    |    |||||||    ||      |     | || |
   CAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAG
        200       210       220       230       240       250       260

    410       420       430       440       450       460       470
   GCGTTGTTGATGGCCTTAATGACCTTGTTCTTGTTGTCGGAGGAACCCAGGAAGGACTTGATCGTGAAGACC
        |  | |  ||  ||| || |      |       ||  |  |||  |   |||  ||   ||| | |
   --AACGACGGTATCCAGAATTACATCCACAAT-------GAATACACCATCATCAACTGCATGAAGAATAAC
        270       280       290              300       310       320

  480       490       500       510       520       530       540
   AGGATGGTAGGGATCAGCAGCTCGGGTTCGAACTCCAACAAAATACCGGCACCCAACAAC-TCAAGGGCATC
              ||||  || |   |||        || |   |  | |      | ||||   |||  ||
   TCTGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAA
   330       340       350       360       370       380       390

 550       560       570       580       590       600       610       620
   CTTGAAGTTGCCCTTCTGTGCCTCGTTGCCGATGTTCAGAGCCAGACCGATGTATGGGACGACGATGGAGAT
     || | |   |        | ||  ||  ||  |        | | | ||   |||  |  || |
   TCTGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTT---ACC
 400       410       420       430       440       450       460

         630       640       650       660       670       680       690
   GTCAGCGATCTTGTCAACAGTG--GACTTCTGGTTAGCCTCAGTAGTGAAGTCTACTAACACCTGCTGAATC
    ||| | ||    | |||| ||   |  |||   |   |     | || | |||| || |  |  |  |  |
   ATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGAC
  470       480       490       500       510       520       530       540

         700       710       720              730       740         750
   CAGCTTACGAACAATGCGGCCTGCACAGGCTTGTT-------GACGTTGTTGATGAAC--TCGGAGGAGAAG
      | |      |  ||   | |   |  | | ||       |||| ||     || |   |  ||   |
   ATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATC
          550       560       570       580       590       600       610

      760       770       780         790       800       810         820
   AAGGTGTAGATCTTAGGCTGCTCCAACAAGG--CTGTGTCAATTGAAGAGGTGAGATTG--ACGTTGTTCTC
   | ||  |   |||    |  || |||||  |  |||| ||| |  || |     ||| |  ||    | |
  TGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAG
      620       630       640       650       660       670       680

      830       840       850       860       870       880       890
  ACCCTCGGGCACCTTCTGAGCGTCTAAGTAGAAGAAGACGTTAAGCTCGTTAACGTCATGCTGCTCGATATC
   |   |    |    ||||  | ||   | |   ||  || | |  |     |   || ||   | |
  TCTTACTCCGAATACCTGAAAGACT-TCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAA
    690       700       710       720       730       740       750

    900       910       920       930       940       950       960
  GGATGTACCGTTGGAGTCGTACTTTGGGATGTA-AGCGTCGTTCTGGATGGTCAGGTTCAGCTTCTCGTCGG
   | ||          | | || ||| |     || | |   | |  || || |||| |  | | |   |||||
  TGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTG--ACTCGTTCC
    760       770       780       790       800       810       820

    970       980       990      1000      1010      1020      1030
  ACAGACCAGGGGCGGACTCGGAGTTGAAGTTTAGGATGACCTGGTCCAGGTCGTTTTCGTAGTTGTTGTTAG
  | | || |     | ||||    | ||       | ||| | || |  | |   | |   | | |
  AAATACAA--CCAGAACTC-----TAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCAT
    830        840              850       860       870       880       890

 1040      1050      1060      1070                1080      1090
  AAGTGACGGTGTCGTCAATCTCCTTAGGAGTGTTGATGTTGT----------CATCGTTGTAACTGTTCTC
   || |         |  ||     |  | || ||| | ||            |   | || ||| ||
  CCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTT
        900       910       920       930       940       950       960

1100      1110      1120      1130      1140        X
  GGAAGCCACGAAGAACAGCTCACCGTTGTTGATCTCGATGCAGATGGACAT
      |  ||| |    |  |   | |   | ||  | | |  |  | |
  CTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCC
      970       980       990      1000      1010 X    1020      1030
```

2. US-09-910-186A-27' (1-1149)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

```
Initial Score      =    37  Optimized Score  =    400  Significance = -0.58
Residue Identity =    40%  Matches           =    464  Mismatches   =   610
Gaps               =    61  Conservative Substitutions            =     0
```

```
   40        50        60        70        80        90       100
  AGGTACGTCTTGACATTCTCGTCGTACTCTCGCAGCTTGTTGATCTTGACCTCGTTGATGAGCTTCATCAGG
                     ||| |  | ||   |     | || | | || |   | ||||| |
                     CTCGAGCCATGGCTCGT-----CTGCTGTCTACCTTCACTGAATACATCAAG
                     X       10              20        30        40

 110       120       130       140       150       160       170       180
  TAGGAGATGGAGGACTCGGTCAGGAACCTGTCGATGTTGTTCATGGCGATGGAGACCTTCTGGTTCAGCTCG
   |    ||  |   |||  ||  |||||||          | ||       ||     | | |   |  | |
  AACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCT
    50        60        70        80        90       100       110

       190       200       210       220       230            240
  TTCTCGATCTGCTTGATATCGTACTTGTTGGTAAGCTCGTTCTTCTCCTCCAG-----GGTGTAGGAGTTGT
  | |   |||        | ||||    |    | |||  ||| ||   ||  | ||     | |  ||  |||
  TCCAAAATC-----AACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCA
 120            130       140       150       160       170       180

 250            260       270       280       290       300        310
  ACTTGGACTC------GATGATGGTCTTGATGGCGTTGACCTGGTTCTGCAGAGCCTGGTAC---ATCTGCT
  |  |||| ||      ||    ||   |  ||  |     |     | | ||   |   ||||  | || ||
  ATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCT
    190       200       210       220       230       240       250

        320       330       340       350       360       370       380
  CCTTTCGCTTGTTGAACTGGGTGTTGATCTTGGTCATCCAGTTCGAGACGATGAAGGAATAGACTTCCTTCC
  ||     ||| | || | |  |  ||  |   ||| |    ||     ||  || ||||| ||    | ||
  CCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCA
 260       270       280       290       300       310       320       330

      390          400       410       420       430       440       450
```

```
  ACTTCTCGTCACGC---TCCTTCAGGGCGTTGTTGATGGCCTTAATGACCTTGTTCTTGTTGTCGGAGGA-A
  ||| |  |  |  |  ||     ||    | |  ||  ||         |  ||| |     | |||| |
  ACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACA
        340       350       360       370       380       390       400

             460       470       480         490       500       510
  CCCAGGAA---GGACTTGATCGTGAAGACCAGGATGGTAGG--GATCAGCAGCTCGGGTTCGAACTCCAACA
  | ||||||      ||    |  || |  | |   |   |  ||||| || ||| |  |  | |     |
  CTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCT
      410       420       430       440       450       460       470

 520       530       540       550       560       570       580       590
  AAATACCGGCACCCAACAACTCAAGGGCATCCTTGAAGTTGCCCTTCTGTGCCTCGTTGCCGATGTTCAGAG
    ||    |   ||| || |   |          || |      |||    |      |   || ||
  GGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACC
     480       490       500       510       520       530       540

        600       610       620       630       640       650       660
  CCAGACCGATGTATGGACGACGATGGAGATGTCAGCGATCTTGTCAACAGTGGACTTCTGGTTAGCCTCAG
   | |||||| |     | |   || |  ||  || |  |  ||||     |    |   |  |
  AGAAACCGATCT-----CCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTG
    550              560       570       580       590       600       610

      670       680       690       700       710       720       730
  TAGTGAAGTCTACTAACACCTGCTGAATCCAGCTTACGAACAATGCGGCCTGCACAGGCTTGTTGACGTTGT
  | ||||     ||   || |   ||   |   | | | |  | || |    |   |   |   | |    |
  TCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAAT
     620       630       640       650       660       670       680

    740       750       760       770       780       790       800
  TGATGAACTCGGAGGAGAAGAAGGTGTAGATCTTAGGCTGCTCCAACAAGGCT-GTGTCAATTGAAGAGGTG
    | || || | | || || ||         ||  | |  | ||  || |   || | || | |    | ||
  CAAAGACCT-GTACGACAACCAG--TCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTA
    690       700        710       720       730       740       750

    810       820       830       840       850             860
  AGATTGACGTTGTT--CTCACCCTCGGGCACCTTCTGAGCGTCTAAGTAGAAG------AAGACGTTAAGCT
   ||   ||  |  |   |         | ||  || || |  || || || |     | |  | || |
  CGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCG
     760       770       780       790       800       810       820

 870       880       890       900          910       920       930
  CGTTAACGTCATGCTGCTCGATATCGGATGTACCGT--TGGAGTCGTACTTTGGGATGTAAGCGTC---GTT
  || | || |      |||   | |    |  || | ||  ||    |  || |       || | | ||   ||
  CGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTA
    830       840       850       860       870       880       890

    940       950       960        970       980       990      1000
  CTGGATGGTCAGGTTCAGCTTCTCGTCGGAC-AGACCAGGGGCGGACTCGGAGTTGAAGTTTAGGATGACCT
  | |       ||  |||| | ||  |    ||  | |  |   |     |   | |      | |||| |
  CCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCG
 900       910       920       930       940       950       960       970

 1010      1020      1030      1040      1050      1060      1070
  GGTCCAGGTCGTTTTCGTAGTTGTTGTTAGAAGTGACGGTGTCGTCAATCTCCTTAGGAGTGTTGATGTTGT
   ||  |  ||  | | ||||||    | |   || || | | |       |      | || |||| |
  TGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGA
          980       990      1000      1010      1020      1030      1040

1080      1090      1100      1110                1120      1130      1140
  CATCGTTGTAACTGTTCTCGGAAGCCACGAAG-----AACAGCTCACCGTTGTTGATCTCGATGCAGATGGA
   |   |  | ||| ||| | || || || |      ||    || | | |  |  |   ||        | | |
  AAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAA
      1050      1060      1070      1080      1090      1100      1110

   X
  CAT
  |
  CGACCAGGGTATCACTAACAAAT
   1120      1130
```

3. US-09-910-186A-27' (1-1149)

```
  US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =      37  Optimized Score   =     400  Significance = -0.58
Residue Identity  =     40%  Matches           =     464  Mismatches   =   610
Gaps              =      61  Conservative Substitutions                =     0

   40        50        60        70        80        90       100
  AGGTACGTCTTGACATTCTCGTCGTACTCTCGCAGCTTGTTGATCTTGACCTCGTTGATGAGCTTCATCAGG
                       |||  |  | ||   |      |  || |  | || |     | ||||| |
                      CTCGAGCCATGGCTCGT-----CTGCTGTCTACCTTCACTGAATACATCAAG
                      X       10             20        30        40

110       120       130       140       150       160       170       180
  TAGGAGATGGAGGACTCGGTCAGGAACCTGTCGATGTTGTTCATGGCGATGGAGACCTTCTGGTTCAGCTCG
   |    ||  |   |||  ||  |||||||         | ||      ||     | | |    |  | |
  AACATCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCT
   50        60        70        80        90       100       110

        190       200       210       220       230            240
  TTCTCGATCTGCTTGATATCGTACTTGTTGGTAAGCTCGTTCTTCTCCTCCAG-----GGTGTAGGAGTTGT
  | |   |||      | ||||    |   | |||  ||| ||   ||  | ||     | |  ||  |||
  TCCAAAATC-----AACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCA
120            130       140       150       160       170       180

 250             260       270       280       290       300          310
  ACTTGGACTC------GATGATGGTCTTGATGGCGTTGACCTGGTTCTGCAGAGCCTGGTAC---ATCTGCT
  |  |||| ||       ||    ||  |  ||  |    |     | | ||   |   ||||   | || ||
  ATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCT
   190       200       210       220       230       240       250

        320       330       340       350       360       370       380
  CCTTTCGCTTGTTGAACTGGGTGTTGATCTTGGTCATCCAGTTCGAGACGATGAAGGAATAGACTTCCTTCC
  ||     ||| | || | |  |   ||  |   ||| |    ||     ||  || ||||| ||   | ||
  CCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCA
 260       270       280       290       300       310       320       330

      390          400       410       420       430       440       450
  ACTTCTCGTCACGC---TCCTTCAGGGCGTTGTTGATGGCCTTAATGACCTTGTTCTTGTTGTCGGAGGA-A
  ||| |  |  |  |   ||     ||    | |   ||  ||         |  ||| |     | |||| |
  ACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACA
         340       350       360       370       380       390       400

           460       470       480         490       500       510
  CCCAGGAA---GGACTTGATCGTGAAGACCAGGATGGTAGG--GATCAGCAGCTCGGGTTCGAACTCCAACA
  | ||||||     ||    |  || |  | |  |   |  |  ||||| || ||| |  |  | |     |
  CTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCT
       410       420       430       440       450       460       470

 520       530       540       550       560       570       580       590
  AAATACCGGCACCCAACAACTCAAGGGCATCCTTGAAGTTGCCCTTCTGTGCCTCGTTGCCGATGTTCAGAG
    ||    |   ||| || |   |           || |      |||    |      |   || ||
  GGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACC
     480       490       500       510       520       530       540

         600       610       620       630       640       650       660
  CCAGACCGATGTATGGGACGACGATGGAGATGTCAGCGATCTTGTCAACAGTGGACTTCTGGTTAGCCTCAG
    | |||||| |      | |    ||  |  ||  || |  |   ||||      |     |   |    |
  AGAAACCGATCT-----CCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTG
   550            560       570       580       590       600       610

       670       680       690       700       710       720       730
  TAGTGAAGTCTACTAACACCTGCTGAATCCAGCTTACGAACAATGCGGCCTGCACAGGCTTGTTGACGTTGT
  | ||||     ||    || |   ||    |   | | | |  | || |    |   |   |   | |   |
  TCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAAT
      620       630       640       650       660       670       680

     740       750       760       770       780        790       800
  TGATGAACTCGGAGGAGAAGAAGGTGTAGATCTTAGGCTGCTCCAACAAGGCT-GTGTCAATTGAAGAGGTG
    | || || | | || ||  ||      ||  | |  | ||  || |   || | || | |    |  ||
  CAAAGACCT-GTACGACAACCAG--TCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTA
    690        700         710       720       730       740       750

    810         820       830       840       850             860
```

```
   AGATTGACGTTGTT--CTCACCCTCGGGCACCTTCTGAGCGTCTAAGTAGAAG------AAGACGTTAAGCT
    ||   ||  |  |   |         | ||  || || |   || || || |      | |  | ||  |
   CGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCG
    760       770       780       790       800       810       820

 870       880       890       900         910       920       930
   CGTTAACGTCATGCTGCTCGATATCGGATGTACCGT--TGGAGTCGTACTTTGGGATGTAAGCGTC---GTT
   || | || |    |||   | |    |  || | ||  ||    |  || |     || |  | ||   ||
   CGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTA
    830       840       850       860       870       880       890

    940       950       960        970       980       990      1000
   CTGGATGGTCAGGTTCAGCTTCTCGTCGGAC-AGACCAGGGGCGGACTCGGAGTTGAAGTTTAGGATGACCT
   | |      ||  |||| | ||  |    ||  | |  |   |     |    | |      |  |||| |
   CCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCG
  900       910       920       930       940       950       960       970

  1010      1020      1030      1040      1050      1060      1070
   GGTCCAGGTCGTTTTCGTAGTTGTTGTTAGAAGTGACGGTGTCGTCAATCTCCTTAGGAGTGTTGATGTTGT
    ||  |  ||  | | ||||||      | |    || || | |  |       |      | || ||| |
   TGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGA
          980       990      1000      1010      1020      1030      1040

1080      1090      1100      1110           1120      1130      1140
   CATCGTTGTAACTGTTCTCGGAAGCCACGAAG-----AACAGCTCACCGTTGTTGATCTCGATGCAGATGGA
    |   |  |  ||| ||| | || ||  || |     ||    || | | |  |  |   ||     | | |
   AAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAA
       1050      1060      1070      1080      1090      1100      1110

     X
   CAT
   |
   CGACCAGGGTATCACTAACAAAT
     1120      1130
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-28.res made by bobryen on Thu 7 Nov 102 14:37:06-PST.

Query sequence being compared:US-09-910-186A-28 (1-382)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

     Results of the initial comparison of US-09-910-186A-28 (1-382) with:
       File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -    **                                                  *
S    0-------------------------------------------------------------
      |     ||     |     |     |      |     |     |      |     |
SCORE 0    20|    40    59    79     99   119   138    158   178
STDEV        0                              1

                              PARAMETERS

Similarity matrix      PAM-150    K-tuple                  1
Threshold level of sim.   16%
Mismatch penalty            1     Joining penalty         20
Gap penalty              5.00     Window size            382
Gap size penalty         0.05
Cutoff score                1
Randomization group         0
                              SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                           69          15          93.83

Times:                   CPU                    Total Elapsed
                   00:00:00.00                  00:00:00.00

Number of residues:                     1704
Number of sequences searched:              3
Number of scores above cutoff:             3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                           Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
--------------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U    850   178   270   1.16   0
                  ****  0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U    415    17   175  -0.55   0
  3. US-08-123-975A-5 Sequence 5, Application U    439    14   173  -0.59   0


1. US-09-910-186A-28 (1-382)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    178  Optimized Score   =    270  Significance =  1.16
Residue Identity  =    41%  Matches           =    157  Mismatches   =   185
Gaps              =      7  Conservative Substitutions               =    33

     X       10        20        30        40        50        60        70
     MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNNYENDLDQVILNFNSESAPGLSDEKLNLTIQ
       |||:: | :|||:|  ||: ||     :    |       :      ||     |   |  |
    APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLTD
     X      10        20        30        40        50        60        70

           80        90       100       110       120       130       140
    NDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSSEFINNVNK
        :| |:      |      |  :| || :|  |     : |||| | |||   |:| ||| ::|   ||
    FNVDVPVYEKQPA--IKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTANK
          80          90       100       110       120       130       140

        150       160       170       180       190       200       210
    PVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVVPYIGLALNIGNEAQKGNFKDALELLGAGILLEFE
     | |:||  |: |:  ||  |||   | ||||||| :|||||||||:|||  ||||  | |  || |||||
    VVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLEFI
         150       160       170       180       190       200       210

      220       230       240       250       260       270       280
    PELLIPTILVFTIKSFLGSSDNKNKVIKAINNALKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQ
    |||||| :  |   |:    |||||:|| | |||  | ||| : |  ||: |:  :||||   || || ||
    PELLIPVVGAFLLESYI---DNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKALN
       220       230          240       250       260       270       280

    290       300       310       320       330       340       350
    NQVNAIKTIIESKYNSYTLEEKNELTNKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINK
     |  |   ||  :|| |   ||       |   |   ||  :  |  ||  |    |:|||||      : |
    YQAQALEEIIKYRYNIYSEKEKSNI--NIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
        290       300         310       320       330       340       350

  360       370       380 X
    LREYDENVKTYLLNYIIQHGSIL
    | ::|   |  |||||      |
    LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMP
        360       370   X 380       390


2. US-09-910-186A-28 (1-382)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     17  Optimized Score   =    175  Significance = -0.55
Residue Identity  =    10%  Matches           =     40  Mismatches   =   320
Gaps              =      6  Conservative Substitutions               =    22

         X       10        20        30        40        50        60
         MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNNYENDLDQVILNFNSESAPGLSDEKLN
           |            :  |    |         :         |      :  |   :      |
    RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
         X  10        20        30        40        50        60        70

     70        80        90       100       110       120       130
    LTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSSEFIN
      |                      |   :   |                 |  :      |:        |
    NSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLN
          80        90       100       110       120       130       140
  140       150       160       170       180       190       200       210
    NVNKPVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVVPYIGLALNIGNEAQKGNFKDALELLGAGIL
    |    : : |        |       |     |   |    :      |       |           :|||
    NSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGIL
       150       160       170       180       190       200       210

          220       230       240        250       260       270       280
    LEFEPELLIPTILVFTIKSFLGSSDNKNKVIKAINNA-LKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQM
     :|  : |      :    :          :       ||           :  |           |
    KDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGN
     220       230       240       250       260       270       280

         290       300       310       320            330       340
    YQALQNQVNAIKTIIESKYNSYTLEEKNELTNKYDIKQI-----ENELNQKVSIAMNNIDRFLTESSISYLM
              :   :  |   | |           |           | | |     |
    KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQD
   290       300       310       320       330       340       350       360

  350       360       370       380 X
    KLINEVKINKLREYDENVKTYLLNYIIQHGSIL
       |::       :    |    |
    NNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGER
           370       380       390  X    400       410


3. US-09-910-186A-28 (1-382)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     14  Optimized Score  =    173  Significance = -0.59
Residue Identity =    11%  Matches          =     50  Mismatches   =   296
Gaps             =     51  Conservative Substitutions              =    29

       X    10        20        30        40        50        60
    MSICIEINNGELFFVASENSYNDDNINTPKEIDDTVTSNNNYENDLDQVILNFNSESAPGLSDEK-------
           |   |  :     | | |          |      |           |  :
       FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNS
       X       10        20        30        40        50        60

         70        80        90       100       110       120       130
    --LNLTIQNDAYIPKYDSNGTSDIEQHDVNELNVFFYLDAQKVPEGENNVNLTSSIDTALLEQPKIYTFFSS
      |   :     ||||   |       :    |      : |:    | :  |               ||
    VFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWT----LIDINGKTKSVFFEY
   70        80        90       100       110       120           130

      140       150       160       170       180       190       200
    EFINNVNKPVQAALFVSWIQQVLVDFTTEANQKSTVDKIADISIVVPYIGLALNIGNEAQKGNFKDALELLG
         :   :    ||                      | ||  |:           :  :  |
    NIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSI
    140       150       160       170       180       190       200

    210                     220       230       240
    AGILLEFEP--------------ELLIPTILVFTIKSFLGSSDNKNKVIKAINNA-----------------
        |                         | :    ::  : |||  ||    :
    FNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKY
  210       220       230       240       250       260       270       280

   250       260       270       280       290              300       310
    LKERDEKWKEVYSFIVSNWMTKINTQFNKRKEQMYQALQNQVNAIKTII-------ESKYNSYTLEEKNELT
       ||    | :          ||    :: :  |    |     :          | |       :  |
    INYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFY
          290       300       310       320       330       340       350

        320       330       340       350       360       370       380 X
    NKYDIKQIENELNQKVSIAMNNIDRFLTESSISYLMKLINEVKINKLREYDENVKTYLLNYIIQHGSIL
    |   ||  :              :    |       :      :         :    |  :      |
    NTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLG
        360       370       380       390       400       410       420 X

    CNWQFIPKDEGWTE
      430
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29.res made by bobryen on Thu 7 Nov 102 14:49:57-PST.


Query sequence being compared:US-09-910-186A-29 (1-1227)
Number of sequences searched:                       3
Number of scores above cutoff:                      3

      Results of the initial comparison of US-09-910-186A-29 (1-1227) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                                                        *
S    0----------------------------------------------------------------------
       |      |      |      |      |   |  ||  |  ||  |  |  |   |   |  |
SCORE  0      6     12     18     24   | 29|  | 35|  | 41  |  47   | 53
STDEV                             -9  -8  -7 -6  -5 -4 -3 -2  -1   0

                               PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                            SEARCH STATISTICS

Scores:                   Mean        Median       Standard Deviation
                            51            49             2.89

Times:                    CPU                      Total Elapsed
                    00:00:00.00                    00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name      Description                  Length Score Score  Sig. Frame
------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338    53   412   0.69   0
   2. US-08-123-975A-1 Sequence 1, Application U   1338    53   412   0.69   0
                  ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351    48   412  -1.04   0

1. US-09-910-186A-29 (1-1227)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     53  Optimized Score   =    412  Significance =  0.69
Residue Identity  =    41%  Matches           =    499  Mismatches   =   633
Gaps              =     64  Conservative Substitutions               =     0

            50        60  X     70        80         90       100       110
      TTATTCTTTGTCGCTTCCGAGTCAAGCTACAACGAGAACGATAT-TAACACACCTAAAGAGATTGACGATAC
                           || ||| |   |  |   | | | || |    || || | ||  |  | |
                          CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                          X       10        20        30        40        50

          120       130       140       150       160       170       180
      TACCAACCTAAACAACAACTACCGGAACAACTTGGATGAGGTTATTTTGGATTACAACTCACAGACCATCCC
       | |||      || |    ||| |  | ||   ||      |    ||    ||   || |    |    |
      CATCAATACCTCCATCCTGAACCTGCGCTAC---GAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTC
            60        70        80           90       100       110       120

        190       200       210       220          230       240       250
      TCAAATTTCCAACCGTACCTTAAACACTCTTGTCCAAGACAAC--TCCTACGTTCCAAGATACGATTCTAAC
        ||||   || | || |   |   |   | |  |    | ||     |  | ||||       | |||
      CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCT--G
            130       140       150       160       170       180       190

        260       270       280       290        300       310       320
      GGTACCTCAGAGATCGAGGAGTATGATGTTGTTGACT-TTAACGTCTTTTTCTATTTGCATGCCCAGAAGGT
      |   | ||  | ||||| |    | ||  ||  || |  || ||| |    || | ||  | |  | |
      GAATCTTCCAAAATCGAAG----TTATCCTGAAGAATGCTATCGTATACAACTCTATG--TACGAAAACTTC
            200       210           220       230       240         250

       330       340       350       360       370       380       390
      GCCAGAAGGTGAAACCAACATCTCATTGACTTCTTCCATTGATACCGCCTTGTTGGAAGAGTCCAAGGATAT
       |||     |        | | ||    | | |||| | |    ||  ||   || |  |     |    ||
      TCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACT----CCATCTCTCTGAACAATGAATACACCAT
      260       270       280       290           300       310       320

     400       410       420       430       440       450       460       470
      CTTCTTTTCTTCGGAGTTTATCGATACTATCAACAAGCCTGTCAACGCCGCTCTGTTCATTGATTGGATTAG
      | ||   |    |||    |    |  |   ||     || | |||  || |    ||||   | |  |  |
      CATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCAT--CTGGACTCTG
        330       340       350       360       370       380         390

             480        490       500       510       520        530       540
      CAAGGTCATCA-GAGATTTTACCACTGAAGCTACTCAAAAGTCCACTGTTGAT-AAGATTGCTGACATCTCT
      || |    ||| || ||   ||  |      || |||||    | | | |||| || ||  |||||
      CAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGAC------
        400       410       420       430       440       450       460

             550       560       570         580       590       600       610
      TTGATTGTCCCCTATGTCGGTCTTGCTTTGAACATCATT--ATTGAGGCAGAAAAGGGTAACTTTGAGGAGG
      |  ||    | ||   ||    || |  | | || || |    |||   |    |   |     | |   |
      TACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGC
            470       480       490       500       510       520       530

             620       630       640       650       660       670       680
      CTTTTGAATTGTTGGGAGTTGGTATTTTGTTGGAGTTTGTTCCAGAACTTACCATTCCTGTCATTTTAGTTT
      | | |||       | |   | | |    |  | ||    ||||   |||   ||  |      || |   |
      CGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCA-CGCTTCTAATAACATCATGTTCAAACT
          540       550       560       570        580       590       600

              690       700       710       720       730       740       750
      TTACG---ATCAAGTCCTACATCGATTCATACGAGAACAAGAATAAAGCAATTAAAGCTATTAACAACTCCT
        |||    ||  | |   || || | ||| |  || ||  ||||   ||||     | |  || ||||
    GGACGGTTGTCGTGACACTCACCGCTACAT-CTGGATCA--AATACTTCAATCTGTTCGACAAAGAACTGAA
       610       620       630        640         650       660       670

          760       770       780       790       800       810       820
    TGATCGAAAGAGAGGCTAAGTGGAAGGAAATCTACTCATGGATTGTATCAAACTGGCTTACTAGAATTA--A
     ||   | | |      |  || | |  || |    ||    | |||||      |  | || |  | |  |
    CGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTA
        680       690       700       710       720       730       740

          830       840       850       860       870       880       890
    CACTCAATTTAACAAGAGAAAGGAGCAAATGTACCAGGCTCTGCAAAACCAAGTCGATGCTATCAAGACTGC
    |   || |   ||||     |  |     || | | |      |  ||| ||  || ||   |||| | ||
    CCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGT
      750       760       770       780       790       800       810

              900       910       920            930       940       950
    AATT------GAATACAAGTACAACAACTATAC-----TTCCGATGAGAAGAACAGACTTGAATCTGAATAC
    |  |      |  |||| ||||   ||   | |      | |  | |  |  ||  || |  | ||||  ||
    AGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGA--AC
    820       830       840       850       860       870       880

       960       970       980       990      1000      1010      1020
    AATATCAACAACATTGAAGAAGAGTTGAACAAGAAAGTTTCTTTGGCTATGAAGAATATCGAAAGATTTATG
      |  |    ||  ||      | || | ||  ||    |    | ||   || ||   | | |   ||
    TCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGC
    890       900       910       920       930       940       950

    1030        1040      1050        1060      1070      1080      1090
    ACCGA--ATCCTCTATCTCTTACTTGATGAAGTT--GATCAATGAGGCCAAGGTTGGTAAGTTGAAGAAGTA
    | | |  ||| | |||  | |   || || ||||  || ||| ||   |    | | ||            |
    AACAATGATCGTGTAT-ACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA
  960       970        980       990      1000      1010      1020      1030

      1100      1110      1120      1130      1140         1150      1160
    CGATAACCACGTTAAGAGCGATCTGCTGAACTACATTCTCGACCACAG--ATCAATC-CTGGGAGAGCAGAC
     | |      |  |||| |             | || |  |||    |  |||  || | || ||     |
    GGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAAT
          1040      1050      1060      1070      1080      1090      1100

       1170      1180      1190      1200      1210      1220      X
    AAACGAGCTGAGTGATTTGGTTACTTCCACTTTGAACTCCTCCATTCCATTTGAGCTTTCTTAA
     ||      ||  ||   || ||    ||||   || | |   ||     |  ||       |
    GAAATCCAAGAACGACCAGGGTA---TCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGA
        1110      1120         1130      1140      1150      1160  X   1170

    TATCGGTTTCAT
         1180


2. US-09-910-186A-29 (1-1227)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =     53  Optimized Score =    412  Significance =  0.69
Residue Identity  =    41%  Matches         =    499  Mismatches   =   633
Gaps              =     64  Conservative Substitutions          =     0

          50       60   X     70        80         90       100       110
    TTATTCTTTGTCGCTTCCGAGTCAAGCTACAACGAGAACGATAT-TAACACACCTAAAGAGATTGACGATAC
                         || ||| |   |  |   | | | || |    || || | ||  |  | |
                        CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACAT
                        X       10        20        30        40        50

        120       130       140       150       160       170       180
    TACCAACCTAAACAACAACTACCGGAACAACTTGGATGAGGTTATTTTGGATTACAACTCACAGACCATCCC
     | |||      || |    ||| |  | ||   ||      |    ||    ||   || |    |    |
    CATCAATACCTCCATCCTGAACCTGCGCTAC---GAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTC
          60        70        80           90       100       110       120

      190       200       210       220         230       240       250
    TCAAATTTCCAACCGTACCTTAAACACTCTTGTCCAAGACAAC--TCCTACGTTCCAAGATACGATTCTAAC
      ||||   || | || |   |   |   | |  |    | ||     |  | ||||       | |||
    CAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCT--G
          130       140       150       160       170       180       190
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      260       270       280       290        300       310       320
    GGTACCTCAGAGATCGAGGAGTATGATGTTGTTGACT-TTAACGTCTTTTTCTATTTGCATGCCCAGAAGGT
    |   | ||  | ||||| |    | ||  ||  || |  || ||| |    || | ||  | |  | |
    GAATCTTCCAAAATCGAAG----TTATCCTGAAGAATGCTATCGTATACAACTCTATG--TACGAAAACTTC
          200       210           220       230       240         250

     330       340       350       360       370       380       390
    GCCAGAAGGTGAAACCAACATCTCATTGACTTCTTCCATTGATACCGCCTTGTTGGAAGAGTCCAAGGATAT
     |||     |        | | ||    | | |||| | |    ||  ||   || |  |     |    ||
    TCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACT----CCATCTCTCTGAACAATGAATACACCAT
    260       270       280       290           300       310       320

   400       410       420       430       440       450       460       470
    CTTCTTTTCTTCGGAGTTTATCGATACTATCAACAAGCCTGTCAACGCCGCTCTGTTCATTGATTGGATTAG
    | ||   |    |||    |    |  |   ||     || | |||  || |    ||||   | |  |  |
    CATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCAT--CTGGACTCTG
      330       340       350       360       370       380         390

           480        490       500       510       520        530       540
    CAAGGTCATCA-GAGATTTTACCACTGAAGCTACTCAAAAGTCCACTGTTGAT-AAGATTGCTGACATCTCT
    || |    ||| || ||   ||  |      || |||||    | | | |||| || ||  |||||
    CAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGAC------
      400       410       420       430       440       450       460

           550       560       570         580       590       600       610
    TTGATTGTCCCCTATGTCGGTCTTGCTTTGAACATCATT--ATTGAGGCAGAAAAGGGTAACTTTGAGGAGG
    |  ||    | ||   ||    || |  | | || || |    |||   |    |   |     | |   |
    TACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGC
          470       480       490       500       510       520       530

           620       630       640       650       660       670       680
    CTTTTGAATTGTTGGGAGTTGGTATTTTGTTGGAGTTTGTTCCAGAACTTACCATTCCTGTCATTTTAGTTT
    | | |||       | |   | | |    |  | ||    ||||   |||   ||  |      || |   |
    CGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCA-CGCTTCTAATAACATCATGTTCAAACT
        540       550       560       570        580       590       600

            690       700       710       720       730       740       750
    TTACG---ATCAAGTCCTACATCGATTCATACGAGAACAAGAATAAAGCAATTAAAGCTATTAACAACTCCT
      |||    ||  | |   || || | ||| |  || ||  ||||   ||||     | |  || ||||
    GGACGGTTGTCGTGACACTCACCGCTACAT-CTGGATCA--AATACTTCAATCTGTTCGACAAAGAACTGAA
       610       620       630        640         650       660       670

          760       770       780       790       800       810       820
    TGATCGAAAGAGAGGCTAAGTGGAAGGAAATCTACTCATGGATTGTATCAAACTGGCTTACTAGAATTA--A
     ||   | | |      |  || | |  || |    ||    | |||||      |  | || |  | |  |
    CGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTA
        680       690       700       710       720       730       740

          830       840       850       860       870       880       890
    CACTCAATTTAACAAGAGAAAGGAGCAAATGTACCAGGCTCTGCAAAACCAAGTCGATGCTATCAAGACTGC
    |   || |   ||||     |  |     || | | |      |  ||| ||  || ||   |||| | ||
    CCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGT
      750       760       770       780       790       800       810

              900       910       920            930       940       950
    AATT------GAATACAAGTACAACAACTATAC-----TTCCGATGAGAAGAACAGACTTGAATCTGAATAC
    |  |      |  |||| ||||   ||   | |      | |  | |  |  ||  || |  | ||||  ||
    AGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGA--AC
    820       830       840       850       860       870       880

       960       970       980       990      1000      1010      1020
    AATATCAACAACATTGAAGAAGAGTTGAACAAGAAAGTTTCTTTGGCTATGAAGAATATCGAAAGATTTATG
      |  |    ||  ||      | || | ||  ||    |    | ||   || ||   | | |   ||
    TCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGC
    890       900       910       920       930       940       950

    1030        1040      1050        1060      1070      1080      1090
    ACCGA--ATCCTCTATCTCTTACTTGATGAAGTT--GATCAATGAGGCCAAGGTTGGTAAGTTGAAGAAGTA
    | | |  ||| | |||  | |   || || ||||  || ||| ||   |    | | ||            |
    AACAATGATCGTGTAT-ACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA
  960       970        980       990      1000      1010      1020      1030
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      1100      1110      1120      1130      1140         1150      1160
    CGATAACCACGTTAAGAGCGATCTGCTGAACTACATTCTCGACCACAG--ATCAATC-CTGGGAGAGCAGAC
     | |      |  |||| |             | || |  |||    |  |||  || | || ||     |
    GGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAAT
          1040      1050      1060      1070      1080      1090      1100

       1170      1180      1190      1200      1210      1220       X
    AAACGAGCTGAGTGATTTGGTTACTTCCACTTTGAACTCCTCCATTCCATTTGAGCTTTCTTAA
     ||      ||  ||   || ||    ||||   || | |   ||     |  ||       |
    GAAATCCAAGAACGACCAGGGTA---TCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGA
        1110      1120         1130      1140      1150      1160  X   1170

    TATCGGTTTCAT
         1180


3. US-09-910-186A-29 (1-1227)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    48  Optimized Score =    412  Significance = -1.04
Residue Identity  =   41%  Matches         =    483  Mismatches   =   620
Gaps              =    68  Conservative Substitutions              =     0

            80        90       100       110       120       130       140
    ACAACGAGAACGATATTAACACACCTAAAGAGATTGACGATACTACCAACCTAAACAACAACTACCGGAA-C
                        |   ||    | |   || || |    | ||| ||||| | |  || ||| |
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X        10        20        30        40        50

          150       160       170       180       190       200       210
    AACTTGGATGAGGTTATTTTGGATTACAACTCACAGACCATCCCTCAAATTTCCAACCGTACCTTAAACACT
      | |     ||   |   |    |  | ||  | |   |     | ||  |  ||   |||     ||  |
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATAC----GACGGT
          60        70        80        90       100       110           120

        220       230       240       250       260       270
    CTTGTCCAAGACAACTCCTACGTTCCAAGATACGATTCTAACGGTACCTCAGAGATCGAGG------AGTAT
     |||  |   |  ||    ||      | |      |||  || || |||  |||||   |      || ||
    GTTGAACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAAT
           130       140       150       160       170       180       190

  280       290       300       310       320       330       340       350
    GATGTTGTTGACTTTAACGTCTTTTTCTATTTGCATGCCCAGAAGGTGCCAGAAGGTGAAACCAACATCTCA
     |     |   |||  ||| | | |||   | |  | | | |       | | |   | | ||   |   ||
    CAGAACATCATCTTCAACTCCGTATTC--CTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
         200       210         220       230       240       250       260

          360       370       380       390       400       410       420
    TTGACTTCTTCCATTGATACCGCCTTGTTGGAAGAGTCCAAGGATATCTTCTTTTCTTCGGAGTTTATCGAT
       ||  |    ||  | |    | |     | || | ||     ||| ||   |    | ||  || |  |
    AGAACGAC-GGTATCCAGAATTACATCCACAATGAATACA---CCATCATCAACTGCATGAAGAATAACTCT
         270        280       290       300          310       320       330

        430       440       450       460       470       480       490
    ACTATCAACAAGCCTGTCAACGCCGCTCTGTTCATTGATTGGATTAGCAAGGTCATCAGAGATTTTACCACT
      |   || |   |  ||  ||     |   ||||        | | | |  ||| | |  |    |   ||
    GGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCT
           340       350       360       370       380       390       400

      500       510       520       530       540       550       560
    GAAGCTACTCAAAAGTCCACTGTTGATAAGATTGCTGACATCTCTTTGATTGTCCCCTATGTCGGTCTTGCT
    | |       || |   ||    |||  | ||  ||||          ||    |  |   | | ||||  |
    GTATTCTTCGAATACAACATCCGTGAAGACATCTCTGA----------ATACATCAATCGCTGGTTCTTCGT
         410       420       430       440                 450       460

    570       580       590       600       610       620       630
    TTGAACATCATTATTGAGGCAGAAAAGGGTAACTTTGAGGAGGCTTTTGAATTGTTGGGAGTTGGTATTTTG
    |  | |||||  | | |     | || | |||  |  |         | ||    ||| |  |  ||
    T--ACCATCACCAATAACCTGAACAATGCTAAAATCTACATCAACGGTAAA---CTGGAATCTAATACCGAC
         470       480       490       500       510           520       530

  640       650       660       670       680       690       700       710
    TTGGAGTTTGTTCCAGAACTTACCATTCCTGTCATTTTAGTTTTTACGATCAAGTCCTACATCGATTCATAC
     |  |     | |  ||| ||| |  |   |      |  | || |   |  |     ||||||||     |
    ATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACC
          540       550       560       570       580       590       600

            720       730       740            750       760       770
    GAGAACA--AGAATAAAGCAATTAAAGCTATTAA-----CAACTCCTTGATCGAAAGAGAGGCTAAGTGGAA
     ||  ||   | || ||  | ||     | || |      ||||   | |    || |  |   ||  || |
    CAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAA-CGGTA
        610       620       630       640       650       660        670

     780       790       800       810         820       830       840
    GGAAATCTACTCATGGATTGTATCAAACTGGCTTACT--AGAATTAACACTCAATTTAACAAGAGAAAGGAG
      | ||| | || |     | ||  | |||    |||   |   |||  | |   |  |||| | | |  |
    CAAGATCCAGTCTTACTCCGAAT--ACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATAC
       680       690         700       710       720       730       740

     850       860       870       880       890       900       910
    CAAATGTACCAGGCTCTGCAAAACCAAGTCGATGCTATCAAGACTGCAATTGAATACAAGTACAACAACTAT
     | |||| | | |||  | || |  || ||  |   |||||       |  || |    |       |
    TATATGTTCAATGCT-GGTAACAAGAACTC--TTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATC
       750        760       770         780       790       800       810

   920       930       940       950       960                 970       980
    ACTTCCGATGAGAAGAACAGACTTGAATCTGAATACAATATCAAC---------AACATTGAAGAAGAGTTG
        |   |   ||  |||  |   | ||| |||||  | | ||          |||| |  ||| ||||
    CTGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTC
        820       830       840       850       860       870       880

               990         1000      1010      1020      1030      1040
    AACA-----AGAAAGT----TTCTTTGGCTATGAAGAATATCGAAAGATTTATGACCGAATCCTCTATCTCT
    | ||      | || |     |||  | | || ||  ||  |     |  ||     || | |     |
    ATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTG
      890       900       910       920       930       940       950

      1050      1060      1070      1080      1090      1100      1110
    TACTTGATGAAGTTGATCAATGAGGCCAAGGTTGGTAAGTTGAAGAAGTACGATAACCACGTTAAGAGCGAT
     ||||  | ||  |||   | ||        ||    |  |  ||| | | | | ||  | |   | |    |
    GACTTCTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTT
    960       970       980       990      1000      1010      1020

    1120      1130      1140      1150      1160      1170      1180
    CTGCTGAACTACATTCTCGACCACAGATCAATCCTGGGAGAGCAGACAAACGAGCTGAGTGATTTGGTTACT
     | |||  || |  ||||     | ||  ||  ||   | | ||  || |  |    |   |    |
    TTCCTG-GCTCCGATCTCTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAA--TACGACGAACAG
 1030       1040      1050      1060      1070      1080        1090

  1190      1200      1210      1220      X
    TCCACTTTGAACTCCTCCATTCCATTTGAGCTTTCTTAA
     | || |     | |    | |  ||  ||     | ||
    CCGACCTACTCTTGCCAGCTGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGG
      1100      1110      1120      1130      1140      1150
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> O <
O| |O  IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-29-inv.res made by bobryen on Thu 7 Nov 102 14:50:14-PST.


Query sequence being compared:US-09-910-186A-29’ (1-1227)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-29’ (1-1227) with:
        File : US08123975A.seq
```

complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                               *
N     -
C     -
E     -                                                        *
S    0----------------------------------------------------------------------
      |      |      |      ||  |  ||   |  |  |  ||  |   ||   |  ||     |
SCORE 0      4      8     12|  | 16|   |20   |  24   |  28|   |32|    36
STDEV                      -9 -8  -7  -6   -5 -4  -3   -2  -1   0


                                 PARAMETERS

Similarity matrix      Unitary     K-tuple                      4
Mismatch penalty             1     Joining penalty             30
Gap penalty               5.00     Window size                500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                              SEARCH STATISTICS

Scores:                      Mean        Median      Standard Deviation
                             34          33          2.31

Times:                  CPU                       Total Elapsed
                    00:00:00.00                   00:00:00.00

Number of residues:                      4027
Number of sequences searched:               3
Number of scores above cutoff:              3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                       Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U  1338    36   455   0.87   0
   2. US-08-123-975A-1 Sequence 1, Application U  1338    36   455   0.87   0
   3. US-08-123-975A-6 Sequence 6, Application U  1351    32   372  -0.87   0

1. US-09-910-186A-29’ (1-1227)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score    =     36  Optimized Score =     455  Significance =  0.87
Residue Identity =    42%  Matches         =     549  Mismatches   =   651
Gaps             =     98  Conservative Substitutions              =     0

                        X       10        20        30                40
                        TTAAGAAAGCTCAAATGGAATGGAGGAGTTCAAAGTGGA--------AGTAA
                        | || | | |   ||    ||  |    | ||   || |        |  ||
    CGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAA
        20        30    X   40        50        60        70        80

        50            60        70        80        90       100'       110
    CCAAATCAC----TCAGCTCGTTTGTCTGCTCTCCCAGGATTGATCTGTGGTCGAGAATGTAGTTC-AGCAG
     | ||||||    ||  |  || |  || | || |||  ||  |  |  | || | | |  | ||| | | |
    TCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCG
      90       100       110       120       130       140       150

          120          130       140       150       160         170
    ATCGCTCTTAACGTGGT---TATCGTACTTCTTCAACTTACCAACCTTGGCCTCAT--TGATCAACTTCATC
    ||||     ||   | |     |  |   |||  ||  | ||||  | |   | ||  |||  ||    |||
    ATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATC
   160       170       180       190       200       210       220       230

   180       190       200       210       220       230       240       250
    AAGTAAGAGATAGAGGATTCGGTCATAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAAC
       ||  |      | |      | |       ||  | |   ||     |    ||   |||   | || |
    GTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATC
           240       250       260       270       280       290       300

            260       270       280        290       300       310       320
    TCT-TCTTCAATGTTGTTGATATTGTATTCAG-ATTCAAGTCTGTTCTTCTCATCGGAAGTATAGTTGTTGT
    ||| |   |||||        ||  |   | | ||  ||  |  ||||  |  | | ||||||   ||   |
    TCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGT--TGGAAAGTATCTCTGAACT
         310       320       330       340       350         360       370

            330       340       350       360       370         380
    AC-TTGTATTCAATTGCAGTCTTGATAGCATCGACTTGGTTTTGCAGAGCCTGGTA--CATTTGCTC-----
    ||  || | |||  || | |||  |   ||   |     |    ||| |  | |||  ||  | |||
    ACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
         380       390       400       410       420       430       440

             390       400       410       420       430       440
    ------CTTTCTCTTGTTAAATTGAGTGTTAATTCTAGTAAGCCAGTTTGATACAATCCATGAGTAGAT-TT
             |||||   || ||  |  | |   |||      |||     |   |     ||| ||  |
    TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCA
       450       460       470       480       490       500       510

  450       460       470       480       490       500       510       520
    CCTTCCACTTAGCCTCTCTTTCGATCAAGGAGTTGTTAATAGCTTTAATTGCTTTATTCTTGTTCTCGTATG
       || || |   |   | |  |||| |  ||      ||  |     | | |    ||      ||  ||
    AAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATA
     520       530       540       550       560       570       580

          530       540       550       560       570       580       590
    AATCGATGTAGGACTTGATCGTAAAAACTAAAATGACAGGAATGGTAAGTTCTGGAACAAACTCCAACAAAA
    |    ||||   |  ||  ||       |    |||||   |  |  |  |||||| ||||  |    |
    ACATCATGTTCAAACTGGACG-----GTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCT
   590       600            610       620       630       640       650

        600       610       620       630       640       650       660
    TACCAACTCCCAACAATTCAAAAGCCTCCTCAAAGTTACCCTTTTCTGCCTCAATAATGATGTTCAAAGCAA
       | ||    |||    | |||      ||||||    ||| | |  |  | |     ||  |   | |
    GTTCGACAAAGAACTGAACGAAAAAGAAATCAAAG---ACCTGTACGACAACCAGTCCAATTCTGGTATCCT
    660       670       680       690          700       710       720

    670       680       690       700       710       720       730
  GACCGACATAGGGGACAATCAAAGAGATGTCAGCAATCTTATCAACAGTGGACTTTTGAGTAGCTTCAGTGG
  ||  ||| |  |||   |  |     |   |  ||| |    | |||      |  ||| |   | |  |
  GAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACA------TGCTGAATCTGTACGATCC
     730       740       750       760       770             780       790

  740       750       760       770       780       790       800
  TAAAATCTCTGATGACCTTGCTAATCCAATCAATGAACAGAGCGGCGTTGACAGGCTTGTTGATAGT-ATCG
   || |  |  | |||| |          | ||||| |   | | ||| | ||| |    |  |  ||   ||
  GAACAAATACGTTGACGT---------CAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCG
         800                  810       820       830       840       850

 810       820        830       840        850       860          870
  ATAAACTCCGAAGA-AAAGAAGATATCCTTGGACTCTT-CCAACAAGGCGGTATCAA---TGGAAGAAGTCA
       ||   | ||  |  || || | | || |||||| ||   |  | |||| |||       |  |   |
  TGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAA
      860       870       880       890       900       910       920

    880       890       900       910          920       930       940
  ATGAGATGTTGGTTTCACCTTCTGGCACCTTCTGGGCA---TGCAAATAGAAAAAGACGTTAAAGTCAACAA
  ||  |    ||||  ||    |     | |||    ||     |   || | |   | |||  ||| || ||
  ATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAA
    930       940       950       960       970       980       990

                        950       960        970       980       990
  CA-------------------TCATACTCCTCGATCT-CTGAGGTACCGTTAGAATCGTATCTTGGAACGTA
  ||                     || || |||   ||  ||  | |  | |    ||   ||| | ||
  CAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCC
 1000      1010      1020      1030      1040      1050      1060

       1000      1010      1020      1030      1040      1050      1060
  GGA-----GTTGTCTTGGACAAGAGTGTTTAAGGTACGGTTGGAAATTTGAGGGATGGTCTGTGAGTTGTAA
  |||     ||  |||    || |    | ||| | |      |||     ||||     ||   |  || ||
  GGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAA
1070       1080      1090      1100      1110      1120      1130      1140

     1070      1080      1090      1100      1110        1120      1130
  TCCAAAATAACCTCATCCAAGTTGTTCCGGTAGTTGTTGTTTAGGTTGGTAGTA--TCGTCAATCTCTTTAG
      ||    |   |    | | ||  || ||   |||   | ||||   |  |  ||  |||| ||  ||
  AATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAA
       1150      1160      1170      1180      1190      1200      1210

     1140      1150      1160      1170      1180      1190      1200
  GTGTGTTAATATCGTTCTCGTTGTAGCTTGACTCGGAAGCGACAAAGAATAATTCTGAGTTGTTGACTCTAA
      |||  | ||   || ||   | | | |    ||| ||          | |||| ||| |      |
  ACTGGTTGCT-TCCAACTGGTACAATCGTCAGATCGAA-CGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAG
     1220       1230      1240      1250       1260      1270      1280

   1210      1220      X
  TACACAGACGTGGTGGGGCCAT
  | ||     || |  |     |
  TTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
     1290      1300    X 1310      1320


2. US-09-910-186A-29' (1-1227)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =    36  Optimized Score =      455  Significance =  0.87
Residue Identity  =   42%  Matches         =      549  Mismatches   =   651
Gaps              =    98  Conservative Substitutions                 =     0

                      X       10        20        30                40
                      TTAAGAAAGCTCAAATGGAATGGAGGAGTTCAAAGTGGA--------AGTAA
                      | || | | |   ||    ||  |    | ||   || |        |  ||
  CGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGAACCTGCGCTACGAA
      20        30    X   40        50        60        70        80

      50            60        70        80        90       100        110
  CCAAATCAC----TCAGCTCGTTTGTCTGCTCTCCCAGGATTGATCTGTGGTCGAGAATGTAGTTC-AGCAG
   | ||||||    ||  |  || |  || | || |||  ||  |  |  | || | | |  | ||| | | |
  TCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAAATCAACATCGGTTCTAAAGTTAACTTCGATCCG
    90       100       110       120       130       140       150

        120          130       140       150       160         170
  ATCGCTCTTAACGTGGT---TATCGTACTTCTTCAACTTACCAACCTTGGCCTCAT--TGATCAACTTCATC
  ||||     ||   | |     |  |   |||  ||  | ||||  | |   | ||  |||  ||    |||
  ATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAAGTTATCCTGAAGAATGCTATC
 160       170       180       190       200       210       220       230

 180       190       200       210       220       230       240       250
  AAGTAAGAGATAGAGGATTCGGTCATAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAAC
     ||  |      | |      | |       ||  | |   ||     |    ||   |||   | || |
  GTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATCCCGAAATACTTCAACTCCATC
         240       250       260       270       280       290       300

          260       270       280        290       300       310       320
  TCT-TCTTCAATGTTGTTGATATTGTATTCAG-ATTCAAGTCTGTTCTTCTCATCGGAAGTATAGTTGTTGT
  ||| |   |||||        ||  |   | | ||  ||  |  ||||  |  | | ||||||   ||   |
  TCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGT--TGGAAAGTATCTCTGAACT
       310       320       330       340       350         360       370

          330       340       350       360       370         380
  AC-TTGTATTCAATTGCAGTCTTGATAGCATCGACTTGGTTTTGCAGAGCCTGGTA--CATTTGCTC-----
  ||  || | |||  || | |||  |   ||   |     |    ||| |  | |||  ||  | |||
  ACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGA
       380       390       400       410        420       430       440

           390       400       410        420       430       440
  ------CTTTCTCTTGTTAAATTGAGTGTTAATTCTAGTAAGCCAGTTTGATACAATCCATGAGTAGAT-TT
           |||||   || ||  |  | |   |||      |||     |   |     ||| ||  |
  TGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCA
     450       460       470        480       490       500       510

450       460       470        480       490       500       510       520
  CCTTCCACTTAGCCTCTCTTTCGATCAAGGAGTTGTTAATAGCTTTAATTGCTTTATTCTTGTTCTCGTATG
     || || |   |   | |  |||| |  ||      ||  |     | | |    ||      ||  ||
  AAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTGGGTAACATCCACGCTTCTAATA
   520       530       540        550       560       570       580

        530       540       550        560       570       580       590
  AATCGATGTAGGACTTGATCGTAAAAACTAAAATGACAGGAATGGTAAGTTCTGGAACAAACTCCAACAAAA
  |    ||||   |  ||  ||       |    |||||   |  |  |  |||||| ||||  |    |
  ACATCATGTTCAAACTGGACG-----GTTGTCGTGACACTCACCGCTACATCTGGATCAAATACTTCAATCT
 590       600            610        620       630       640       650

      600       610       620        630       640       650       660
  TACCAACTCCCAACAATTCAAAAGCCTCCTCAAAGTTACCCTTTTCTGCCTCAATAATGATGTTCAAAGCAA
     | ||    |||    | |||      ||||||    ||| | |  |  | |     ||  |   | |
  GTTCGACAAAGAACTGAACGAAAAAGAAATCAAAG---ACCTGTACGACAACCAGTCCAATTCTGGTATCCT
    660       670       680       690          700        710       720

    670       680       690       700       710       720       730
  GACCGACATAGGGGACAATCAAAGAGATGTCAGCAATCTTATCAACAGTGGACTTTTGAGTAGCTTCAGTGG
  ||  ||| |  |||   |  |     |   |  ||| |    | |||      |  ||| |   | |  |
  GAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACA------TGCTGAATCTGTACGATCC
     730       740       750       760       770             780       790

  740       750       760       770       780       790       800
  TAAAATCTCTGATGACCTTGCTAATCCAATCAATGAACAGAGCGGCGTTGACAGGCTTGTTGATAGT-ATCG
   || |  |  | |||| |          | ||||| |   | | ||| | ||| |    |  |  ||   ||
  GAACAAATACGTTGACGT---------CAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCG
         800                  810       820       830       840       850

 810       820        830       840        850       860          870
  ATAAACTCCGAAGA-AAAGAAGATATCCTTGGACTCTT-CCAACAAGGCGGTATCAA---TGGAAGAAGTCA
       ||   | ||  |  || || | | || |||||| ||   |  | |||| |||       |  |   |
  TGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAA
      860       870       880       890       900       910       920

    880       890       900       910          920       930       940
  ATGAGATGTTGGTTTCACCTTCTGGCACCTTCTGGGCA---TGCAAATAGAAAAAGACGTTAAAGTCAACAA
  ||  |    ||||  ||    |     | |||    ||     |   || | |   | |||  ||| || ||
  ATACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATGTTGTAGTTAAGAA
```

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      930       940       950       960       970       980       990

                          950       960        970       980       990
    CA-------------------TCATACTCCTCGATCT-CTGAGGTACCGTTAGAATCGTATCTTGGAACGTA
    ||                     || || |||   ||  ||  | |  | |    ||   ||| | ||
    CAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATCCC
   1000      1010      1020      1030      1040      1050      1060

         1000      1010      1020      1030      1040      1050      1060
    GGA-----GTTGTCTTGGACAAGAGTGTTTAAGGTACGGTTGGAAATTTGAGGGATGGTCTGTGAGTTGTAA
    |||     ||  |||    || |    | ||| | |      |||     ||||     ||   |  || ||
    GGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAA
 1070      1080      1090      1100      1110      1120      1130      1140

       1070      1080      1090      1100      1110        1120      1130
    TCCAAAATAACCTCATCCAAGTTGTTCCGGTAGTTGTTGTTTAGGTTGGTAGTA--TCGTCAATCTCTTTAG
        ||    |   |    | | ||  || ||   |||   | ||||   |  |  ||  |||| ||  ||
    AATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAA
         1150      1160      1170      1180      1190      1200      1210

       1140      1150      1160      1170      1180      1190      1200
    GTGTGTTAATATCGTTCTCGTTGTAGCTTGACTCGGAAGCGACAAAGAATAATTCTGAGTTGTTGACTCTAA
        |||  | ||   || ||   | | | |    ||| ||          | |||| |||| |      |
    ACTGGTTGCT-TCCAACTGGTACAATCGTCAGATCGAA-CGTTCCTCTCGCACTCTGGGTTGCTCTTGGGAG
       1220       1230      1240      1250       1260      1270      1280

     1210      1220      X
    TACACAGACGTGGTGGGGCCAT
    | ||     || |  |     |
    TTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
       1290      1300    X 1310      1320


3. US-09-910-186A-29’ (1-1227)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =     32  Optimized Score  =    372  Significance = -0.87
Residue Identity =    42%  Matches          =    450  Mismatches   =   528
Gaps             =     87  Conservative Substitutions              =     0

       200       210    X  220       230       240       250       260
    ATTCGGTCATAAATCTTTCGATATTCTTCATAGCCAAAGAAACTTTCTTGTTCAACTCTTCTTCAATGTTGT
                        ||    ||||    |||| | | || |    ||        |   ||  ||
                        ATGGCTTTCA---ACAAATACAATTCCGAAATCCTGAACAATATCATCCTGA
                        X       10           20        30        40

     270       280       290       300       310       320       330
    TGATATTGTATTCAGATTCAAGTCTGTTCTTCTCATCGGAAGTATAGTTGTTGTACTTGTATTCAATTGCAG
       |    ||   |||    | |||| ||      || |  ||   | || |  | ||| | |  |   | |
    ACCTGCGTTACAAAGACAACAATCTGATCGATCTGTCTG--GTTACGGTGCTAAAGTTGAAGTATACGACGG
   50        60        70        80          90       100       110

   340       350       360       370       380       390       400       410
    TCTTGATAGCATCGACTTGGTTTTGCAGAGCCTGGTACATTTGCTCCTTTCTCTTGTTAAATTGAGTGTTAA
    | ||||    |  |||  |     |   |  |||  || | | |  ||  |||    |||  |  ||||||
    TGTTGAACTGAATGACAAGAACCAGTTCAAACTG--ACCTCTTCCGCTAACTC----TAAGATCCGTGTTAC
  120       130       140       150         160       170           180

           420       430       440       450       460       470
    TTCTAGTAAGCCAGTTTGATACAATCCATGAGTAGATTTCCTTCCACTTAGCCTCTCTTTCGAT--------
    |   | | ||    |    | |||  |   | |      | |  |  ||  | |||   ||  |
    TCAGAATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAA
      190       200       210       220       230       240       250

          480         490       500       510       520       530
    ---CAAGGA--GTTGTTAATAGCTTTAATTGCTTTATTCTTGTTCTCGTATGAATCGATGTAGGACT-----
       |||| |     ||    ||  |||  | |   ||   |   |    || ||  |    | || |
    ATACAAGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTC
    260       270       280       290       300       310       320

     540       550       560       570             580       590       600
    TGATCGTAAAAACTAAAATGACAGGAATGGTAAGTTCTG------GAACAAACTCCAACAAAATACCAACTC
    || | | || | ||  |    | | ||  |||   ||||      || | |  || |    || ||||| ||
    TGGTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATC
  330       340       350       360       370       380       390       400

         610          620       630       640         650        660
    CCAACAATTCAAA---AGCCTCCTCAAAGTTACCCTTTTCTGCCTCAAT--AATGATGTTC-AAAGCAAGAC
       |   ||| ||   | | |||   |||  | |  |   | | |||||     | | |||   | ||  ||
    TGTATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCAC
          410       420       430       440       450       460       470

   670       680       690       700       710       720       730       740
    CGACATAGGGGACAATCAAAGAGATGTCAGCAATCTTATCAACAGTGGACTTTTGAGTAGCTTCAGTGGTAA
    | | |    | |||||   | |     || |||   |    | | |||| | |  | || |  ||      |
    CAATAACCTGAACAATGCTAAAATCTACATCAACGGT----AAACTGGAATCT--AATACCGACATCAAAGA
        480       490       500       510           520       530

           750       760          770       780       790       800
    AATCTCTGATGACCTTGCTAA---TCCAATCAATGAACAGAGCGGCGTTGACAGGCTTGTTGATAGTATCGA
     |||  ||| |   | |||||   |  |||||      |    | || |||||      | ||| ||| | |
    CATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACA------TCGATCGTACCCA
  540       550       560       570       580       590             600

  810       820       830       840       850       860       870       880
    TAAACTCCGAAGAAAAGAAGATATCCTTGGACTCTTCCAACAAGGCGGTATCAATGGAAGAAGTCAATGAGA
         || |       || || || |||   |   | |||||  |   | ||   |    |  || | ||
    GTTCATCTG-------GATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAAC
      610              620       630       640       650       660       670

          890       900          910       920       930       940       950
    TGTTGGTTTCACCTTCTGGCACC---TTCTGGGCATGCAAATAGAAAAAGACGTTAAAGTCAACAACATCAT
     ||        |  |||  | ||   | |  |  |  |   | |   ||  || | | ||  |  | |  ||
    GGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAAT
           680       690       700       710       720       730       740

           960       970       980       990      1000      1010
    ACTCCTCGATCTCTGAGGTACCGTTAGAATCGTATCTTGGAACGTAGGAGTTGTCTTGGACAAGAG------
    |||    | ||  ||  |         | || ||  |   |  | || |    |||  |    | |
    ACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCC
         750       760       770       780       790       800       810

         1020      1030      1040          1050      1060       1070
    -----TGTTTAAGGTACGGTTGGAAATTTGA----GGGATGGTCTGTGAGTTGTA-ATCCAAAATAACCTCA
          |||  |  |||     ||| | | |       |    | | ||  |||| |||    | ||  |||
    TGACTCGTTCCAAATACAACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCA
       820       830       840       850       860       870       880

  1080      1090      1100      1110      1120      1130      1140      1150
    TCCAAGTTGTTCCGGTAGTTGTTGTTTAGGTTGGTAGTATCGTCAATCTCTTTAGGTGTGTTAATATCGTTC
    ||    |   ||    |  |     | ||      | |   | ||   |   ||     |   | |||   |
    TC---ATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACC
        890       900       910       920       930       940       950

          1160      1170      1180      1190      1200      1210      1220
    TCGTTGTAGCTTGACTCGGAAGCGACAAAGAATAATTCTGAGTTGTTGACTCTAATACACAGACGTGGTGGG
    | |   |  ||| |  | ||| |   || |     |    |  |       ||   | | ||| |  |
    TGGACTT--CTTCAACCTGAATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAA
      960         970       980       990      1000      1010      1020

        X
    GCCAT
    ||  |
    GCTTTTCCTGGCTCCGATCTCTGAT
     1030      1040      1050
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-30.res made by bobryen on Thu 7 Nov 102 14:37:36-PST.

Query sequence being compared:US-09-910-186A-30 (1-408)
Number of sequences searched:                        3
Number of scores above cutoff:                       3

     Results of the initial comparison of US-09-910-186A-30 (1-408) with:
       File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -    **                                                        *
S    0---------------------------------------------------------------------
      |      | |    |      |      |      |      |      |      |      |
SCORE 0     19 |  38     57     76     95    114    133    152    171
STDEV          0                                1

                         PARAMETERS

Similarity matrix      PAM-150     K-tuple                    1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty           20
Gap penalty               5.00     Window size              408
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                      SEARCH STATISTICS

Scores:                Mean       Median       Standard Deviation
                        67          15           89.51

Times:                  CPU                    Total Elapsed
                   00:00:00.00                 00:00:00.00

Number of residues:                 1704
Number of sequences searched:          3
Number of scores above cutoff:         3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name     Description                    Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                  ****  1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U    850   171   276   1.16   0
                  ****  0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U    415    18   174  -0.55   0
  3. US-08-123-975A-5 Sequence 5, Application U    439    14   134  -0.59   0


1. US-09-910-186A-30 (1-408)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    171  Optimized Score  =    276  Significance =  1.16
Residue Identity  =    40%  Matches          =    165  Mismatches   =   202
Gaps              =      8  Conservative Substitutions              =    32

      X     10        20        30        40        50        60        70
    MAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTTNLNNNYRNNLDEVILDYNSQTIPQISNRTLNTL
       |  || | | :|||:|   |: :      :    |            | |||                |
      APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESL
      X       10        20        30        40        50        60        70

          80        90       100       110       120       130        140
    VQDNSYVPRYDSNGTSEIEEYDVVDFNVFFYLHAQKVPEGETNISLTSSIDTALLEESKD-IFFSSEFIDTI
       |  || |:      |      :  :| ||:|  |     |||||| | |||   |   ||| ::| |
    TDFNVDVPVYEKQPA--IKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYIKTA
            80          90       100       110       120       130       140

        150       160       170       180       190       200       210
    NKPVNAALFIDWISKVIRDFTTEATQKSTVDKIADISLIVPYVGLALNIIIEAEKGNFEEAFELLGVGILLE
    || | |:||  |:  :: ||  ||    | ||||||||||||:|||||:  |  ||||| |||  |  ||||
    NKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASILLE
           150       160       170       180       190       200       210

      220       230       240       250       260       270       280
    FVPELTIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREAKWKEIYSWIVSNWLTRINTQFNKRKEQMYQA
    |:||| |||:  |   ||||   |||| || | |:|  |  || : |  ||: ||  :||||   || || |
    FIPELLIPVVGAFLLESYID---NKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
         220       230          240       250       260       270       280

    290       300       310       320       330       340       350
    LQNQVDAIKTAIEYKYNNYTSDEKNRLESEYNINNIEEELNKKVSLAMKNIERFMTESSISYLMKLINEAKV
    |  |  |    | |:|| |   ||     ::  | |   ||  :  |  ||  |    |:|||||      |
    LNYQAQALEEIIKYRYNIYSEKEKSNINIDF--NDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAV
          290       300       310         320       330       340       350

  360       370       380       390       400       X
    GKLKKYDNHVKSDLLNYILDHRSILGEQTNELSDLVTSTLNSSIPFELS
     ||  :||  |  ||||| : :  |          |   |    ||:||
    EKLLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEIL
          360       370       380       390       400       410       420


2. US-09-910-186A-30 (1-408)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     18  Optimized Score  =    174  Significance = -0.55
Residue Identity  =     9%  Matches          =     36  Mismatches   =   330
Gaps              =      2  Conservative Substitutions              =    26

                        X      10        20        30        40        50
                        MAPPRLCIRVNNSELFFVASESSYNENDINTPKEIDDTTNLNNNYRNNLDEV
                           |     :    |     |       :         |            :
    SNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSI
         10        20   X    30        40        50        60        70

          60        70        80        90       100       110       120
    ILDYNSQTIPQISNRTLNTLVQDNSYVPRYDSNGTSEIEEYDVVDFNVFFYLHAQKVPEGETNISLTSSIDT
     |      |    |            :       | ||    |  :                 |
    SLNNEYTIINCMENNSGWKVSLNYGEIIW-TLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNS
       80        90        100        110       120       130       140
    130       140       150       160       170       180       190
 ALLEESKDIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEATQKSTVDKIADISLIVPYVGLALNIIIEA
       : |              |  :|     :    :              :      |   :   |
 KIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKD
  150       160       170       180       190       200       210

  200       210       220       230       240       250       260
 EKGNFEEAFELLGVGILLEFVPELTIPVILVFTIKSYIDSYENKNKAIKAINNSLIEREAKWKEIYSWIVSN
   | :           | :      :  : :                    | ||          |:
 FWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKD
220       230       240       250       260       270       280       290

270       280       290       300       310       320       330       340
 WLTRINTQFNKRKEQMYQALQNQVDAIKTAIEYKYNNYTSDEKNRLESEYNINNIEEELNKKVSLAMKNIER
    | |                   |   ::|         :   | |   :     :        |   :
 NIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNL-SQVVVMKSKNDQGITNKCKMNLQDN
        300       310       320       330        340       350       360

        350       360       370       380       390   X   400
 FMTESSISYLMKLINEAKVGKLKKYDNHVKSDLLNYILDHRSILGEQTNELSDLVTSTLNSSIPFELS
    :          | ||      |   :             |  :       |
 NGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
       370       380       390       400       410    X


3. US-09-910-186A-30 (1-408)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =     14  Optimized Score  =    134  Significance = -0.59
Residue Identity =     9%  Matches          =     29  Mismatches   =   246
Gaps             =      2  Conservative Substitutions              =    15

  100       110       120       130       140       150       160
 DFNVFFYLHAQKVPEGETNISLTSSIDTALLEESKDIFFSSEFIDTINKPVNAALFIDWISKVIRDFTTEAT
                           :          :     ||          :          |   :
                     FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSS
                     X       10        20        30        40        50

170       180       190       200       210       220       230       240
 QKSTVDKIADISLIVPYVGLALNIIIEAEKGNFEEAFELLGVGILLEFVPELTIPVILVFTIKSYIDSYENK
   | :        |   | |   :        :        :      :  :         |:
 ANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRG--NRIIWT
       60        70        80        90       100       110         120

        250       260       270       280       290       300       310
 NKAIKAINNSLIEREAKWKEIYSWIVSNWLTRINTQFNKRKEQMYQALQNQVDAIKTAIEYKYNNYTSDEKN
    | :   |         :|   |       |    |  |      |    |
 LIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDG
      130       140       150       160       170       180       190

      320       330       340       350       360       370       380
 RLESEYNINNIEEELNKKVSLAMKNIERFMTESSISYLMKLINEAKVGKLKKYDNHVKSDLLNYILDHRSIL
   :    |                  ||:   |   ||              |            |   |
 DIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPV
    200       210       220       230       240       250       260

    390       400      X
 GEQTNELSDLVTSTLNSSIPFELS
 ||          |
 GEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVR
  270       280       290       300       310
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31.res made by bobryen on Thu 7 Nov 102 14:50:45-PST.

Query sequence being compared:US-09-910-186A-31 (1-1233)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-31 (1-1233) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                          *
N     -
C     -
E     -                                                    *
S    0-----------------------------------------------------------------
      |      |     |      | |   ||   | | |   |   |  | |  | | |   |
SCORE 0      6    11    17  |  23|   |28 |  34   | 40 |  |45 |  51
STDEV                    -9 -8   -7  -6  -5  -4  -3   -2 -1    0

                           PARAMETERS

Similarity matrix        Unitary    K-tuple                    4
Mismatch penalty               1    Joining penalty           30
Gap penalty                 5.00    Window size              500
Gap size penalty            0.33
Cutoff score                   1
Randomization group            0

                        SEARCH STATISTICS

Scores:                  Mean       Median      Standard Deviation
                          49          46             3.46

Times:                   CPU                    Total Elapsed
                     00:00:00.00                00:00:00.00

Number of residues:                4027
Number of sequences searched:         3
Number of scores above cutoff:        3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                           Init.  Opt.
Sequence Name       Description                    Length  Score Score  Sig. Frame
-----------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U     1338     51   427   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U     1338     51   427   0.58    0
               ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U     1351     45   328  -1.15    0

1. US-09-910-186A-31 (1-1233)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     51  Optimized Score    =    427  Significance =  0.58
Residue Identity  =    43%  Matches            =    518  Mismatches   =   599
Gaps              =     84  Conservative Substitutions                =     0

                      X       10        20        30        40         50
                      ATGGCCAAAAATACCGGTAAATCTGAACAGTGTATTATTGTTAATAAT-GAG
                      || | ||| ||| | | |  | |||  || | |   ||  |  | ||| ||
  CTAAAGTTAACTTCGATCCGATCGACAAGAAT-CAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAA
 140       150       160       170        180       190       200

         60        70            80        90          100       110
  GATTTATTTTTCATAGCTA----ATAAAGATAGTTTTTCAAAAGATT---TAGCTAAAGCAGAAACTATAGC
  | | |  |    |  ||||    ||| |  |   | | | |||  ||    | ||    | | | |  || |
  GTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATC
210       220       230       240       250       260       270       280

   120       130         140       150       160       170       180
  ATATAATACACAAAAT--AATACTATAGAAAATAATTTTTCTATAGATCAGTTGATTTTAGATAATGAT--T
      |||||   || |  |   || |  | ||| | |   | ||     | |  ||   | | |||  |  |
  CCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGT
        290       300       310       320       330       340       350

     190       200       210       220       230       240       250
  TAAGCAGTGGCATAGACTTACCAAATGAAAACACAGAACCATTTACAAATTTTGACGACATAGATATCCCTG
  |    |||  |   ||  |||    ||||| ||      |  |     |   | | || ||  |    | ||
  TGGAAAGTATCTCTGAACTAC--GGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
      360       370         380       390       400       410       420

   260       270       280       290       300       310       320
  TGTATATTAAACAATCTGCTTTAAAAAAAATTTTTGTGGATGGAGATAGCCTTTTTGAATATTTACATGCTC
  |     | ||| | |||    | |  || || | ||   |     || | ||   |     ||  |||   |
  TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCG-CTGGATCTTCGTTACCATCACC
      430       440       450       460       470        480       490

 330       340       350       360       370           380       390
  AAACATTTCCTTCTAATATAGAAAATCTACAACTAACGAATTC----ATTAAATGATGCTTTAAGAAATAAT
  ||  ||   ||    |  |  |||||||||| | |  |   ||         |  |  |  |    |||
  AACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTG
     500       510       520       530       540       550       560

   400       410              420          430       440       450
  AATAAAGTCTATACTTTT-------TTTTCTACAAAC---CTTGTTGAAAAAGCTAATACAGTTGTAGGTGC
    |||  || |  ||| |       |  | | |||||      ||||      |    || | |  |  ||
  GGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGG
   570       580       590       600       610       620       630

 460       470         480       490       500        510       520
  TTCACTTTTTGTAAACTG--GGTAAAAGGAGTAATAGATGATTTTA-CATCTGAATCCACACAAAAAAGTAC
   |||  |  |  || |||   |  |||| | | |  ||  |    | ||      |  ||   ||  ||| |
  ATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCC
 640       650       660       670       680       690       700       710

  530       540       550       560        570          580       590
  TATAGATAAAGTTTCAGATGTATCCATAATTATTCCCTATA-TAGGAC---CTGCTTTGAATGTAGGAAATG
   ||      |   | | |    ||     | | | |||  | || |||   | |   |  |||  | |  ||
  AATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTG
         720       730       740       750       760       770       780

    600       610              620                  630         640
  AAACAGCTAAAGAAA-------ATTTTAAAAATG-----------CTTTTGAAATAGGTGGA--GCCGCTAT
   |  | |  || |||       |  | || ||||             ||  |  ||  || |  | |    |
    TACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGT
         790       800       810       820       830       840       850

    650       660       670       680       690       700       710
    CTTAATGGAGTTTATTCCAGAACTTATTGTACCTATAGTTGGATTTTTACATTAGAATCATATGTAGGAAA
      |  ||   |   | |||  |  ||    | || |     |     |   |  | | ||||    | ||||
    GGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAA
       860       870       880       890       900       910       920

  720       730       740       750       760       770       780       790
    TAAAGGGCATATTATTATGACGATATCCAATGCTTTAAAGAAAAGGGATCAAAAATGGACAGATATGTATGG
    ||   | |   | |  | ||| |||||    ||   || ||    | || |  |  |     ||  || |
    TACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATG--TTGTAGTTAAGA
     930       940       950       960       970       980       990

          800       810       820       830       840       850       860
    TTTGATAGTATCGCAGTGGCTCTCAACGGTTAATACTCAATTTTATACAATAAAAGAAAGAATGTACAA---
        | | || ||   |||||  ||| | ||   |  |   | || | || |           | |  ||
    ACAAAGAATACCG-TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATC
    1000       1010      1020      1030      1040      1050      1060

             870       880       890       900       910       920       930
    --TGCTTTAAATAATCAATCACAAGCAATAGAAAAAATAATAGAAGATCAATATAATAGATATAGTGAAGAA
       |   |   |||||  || || | | | | ||  | ||| |  ||||  |  |  |  |     | | |  ||
    CCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGA-AATCCAAGA--ACGACCAGGGTATCACTAACAAA
   1070      1080      1090      1100       1110        1120      1130

           940          950       960       970       980        990
    GATAAAATGAATAT---TAACATTGATTTTAATGATATAGATTTTAAACTTAATCA-AAGTATAAATTTAGC
       |||||||||| |     |||   ||  ||| ||||| | ||| |    |   ||  |||  ||   || |
    TGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATC
    1140      1150      1160      1170      1180      1190      1200

  1000      1010       1020      1030      1040      1050      1060
    AATAAACAATATAGAT-GATTTTATAAACCAATGTTCTATATCATATCTAATGAATAGAATGATTCCATTAG
      |||||    |   |  |  |  || |    |    |  | | | || |   | | |      | | |  || |
    GCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGG
  1210      1220      1230      1240      1250      1260      1270      1280

 1070      1080      1090      1100      1110      1120      1130      1140
    CTGTAAAAAAGTTAAAAGACTTTGATGATAATCTTAAGAGAGATTTATTGGAGTATATAGATACAAATGAAC
      ||  |            |   | ||||||   |  | | ||      |  |||    |  | |  |
    GAGTTCA-----------TCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
                     1290      1300      1310      1320      1330       X

         1150
    TATATTTACTTGATGAA

2. US-09-910-186A-31 (1-1233)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score     =     51  Optimized Score  =     427  Significance =  0.58
Residue Identity  =    43%  Matches          =     518  Mismatches    =   599
Gaps              =     84  Conservative Substitutions                =     0

                        X       10        20        30        40          50
                        ATGGCCAAAAATACCGGTAAATCTGAACAGTGTATTATTGTTAATAAT-GAG
                        || | ||| ||| | | |  | |||  || | |   ||  |  | ||| ||
    CTAAAGTTAACTTCGATCCGATCGACAAGAAT-CAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCGAA
   140       150       160       170        180       190       200

           60        70            80        90          100       110
    GATTTATTTTTCATAGCTA----ATAAAGATAGTTTTTCAAAAGATT---TAGCTAAAGCAGAAACTATAGC
    | | |  |    |  ||||    ||| |  |   | | | |||  ||    | ||    | | | |  || |
    GTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGATCCGTATC
  210       220       230       240       250       260       270       280

     120       130         140       150       160       170       180
    ATATAATACACAAAAT--AATACTATAGAAAATAATTTTTCTATAGATCAGTTGATTTTAGATAATGAT--T
        |||||   || |  |   || |  | ||| | |   | ||     | |  ||   | | |||  |   |
    CCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAAACAATTCTGGT
          290       300       310       320       330       340       350

       190       200       210       220       230       240       250
    TAAGCAGTGGCATAGACTTACCAAATGAAAACACAGAACCATTTACAAATTTTGACGACATAGATATCCCTG
    |    |||  |   ||  ||    ||||| ||      |  |     |   | | || ||  |    | ||
    TGGAAAGTATCTCTGAACTAC--GGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCAAACAGCGTG
        360       370         380       390       400       410       420

     260       270       280       290       300       310       320
    TGTATATTAAACAATCTGCTTTAAAAAAAATTTTTGTGGATGGAGATAGCCTTTTTGAATATTTACATGCTC
    |     | ||| | |||    | |  || || | ||   |     || | ||   |     ||  |||   |
    TTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCG-CTGGATCTTCGTTACCATCACC
        430       440       450       460       470        480       490

   330       340       350       360       370           380       390
    AAACATTTCCTTCTAATATAGAAAATCTACAACTAACGAATTC----ATTAAATGATGCTTTAAGAAATAAT
    ||  ||   ||    |  |  ||||||||||| | |  |   ||         |  |  |  |    |||
    AACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATCTCCAATCTG
       500       510       520       530       540       550       560

     400       410              420          430       440       450
    AATAAAGTCTATACTTTT-------TTTTCTACAAAC---CTTGTTGAAAAAGCTAATACAGTTGTAGGTGC
      |||  || |  ||| |       |  | | |||||      ||||      |    || | |  |  ||
    GGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGCTACATCTGG
     570       580       590       600       610       620       630

   460       470         480       490       500        510       520
    TTCACTTTTTGTAAACTG--GGTAAAAGGAGTAATAGATGATTTTA-CATCTGAATCCACACAAAAAAGTAC
     |||  |  |  || |||   |  |||| | | |  ||  |    | ||      |  ||   ||  ||| |
    ATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCC
   640       650       660       670       680       690       700       710

    530       540       550       560        570          580       590
    TATAGATAAAGTTTCAGATGTATCCATAATTATTCCCTATA-TAGGAC---CTGCTTTGAATGTAGGAAATG
     ||      |   | | |    ||     | | | |||  | || |||   | |   |  |||  | |  ||
    AATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTACATGCTGAATCTG
           720       730       740       750       760       770       780

      600       610              620                  630         640
    AAACAGCTAAAGAAA-------ATTTTAAAAATG-----------CTTTTGAAATAGGTGGA--GCCGCTAT
     |  | |  || |||       |  | || ||||              || |  ||  || |  | |     |
    TACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGT
         790       800       810       820       830       840       850

    650       660       670       680       690       700       710
    CTTAATGGAGTTTATTCCAGAACTTATTGTACCTATAGTTGGATTTTTACATTAGAATCATATGTAGGAAA
      |  ||   |   | |||  |  ||    | || |     |     |   |  | | ||||    | ||||
    GGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAA
       860       870       880       890       900       910       920

  720       730       740       750       760       770       780       790
    TAAAGGGCATATTATTATGACGATATCCAATGCTTTAAAGAAAAGGGATCAAAAATGGACAGATATGTATGG
    ||   | |   | |  | ||| |||||    ||   || ||    | || |  |  |     ||  || |
    TACGCGTCTGGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATACATCAATG--TTGTAGTTAAGA
     930       940       950       960       970       980       990

          800       810       820       830       840       850       860
    TTTGATAGTATCGCAGTGGCTCTCAACGGTTAATACTCAATTTTATACAATAAAAGAAAGAATGTACAA---
        | | || ||   |||||  ||| | ||   |  |   | || | || |           | |  ||
    ACAAAGAATACCG-TCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATCTTGTCTGCTCTGGAAATC
    1000       1010      1020      1030      1040      1050      1060

             870       880       890       900       910       920       930
    --TGCTTTAAATAATCAATCACAAGCAATAGAAAAAATAATAGAAGATCAATATAATAGATATAGTGAAGAA
       |   |   |||||  || || | | | | ||  | ||| |  ||||  |  |  |  |     | | |  ||
    CCGGACGTTGGTAATCTGTCTCAGGTAGTTGTAATGA-AATCCAAGA--ACGACCAGGGTATCACTAACAAA
   1070      1080      1090      1100       1110        1120      1130

           940          950       960       970       980        990
    GATAAAATGAATAT---TAACATTGATTTTAATGATATAGATTTTAAACTTAATCA-AAGTATAAATTTAGC
       |||||||||| |     |||   ||  ||| ||||| | ||| |    |   ||  |||  ||   || |
    TGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATC
    1140      1150      1160      1170      1180      1190      1200
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1000      1010      1020      1030      1040      1050      1060
   AATAAACAATATAGAT-GATTTTATAAACCAATGTTCTATATCATATCTAATGAATAGAATGATTCCATTAG
     |||||    |   |  |  |  || |    |    |  | | |  ||   | |      | | |  || |
   GCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGCACTCTGGGTTGCTCTTGG
1210      1220      1230      1240      1250      1260      1270      1280

1070      1080      1090      1100      1110      1120      1130      1140
   CTGTAAAAAAGTTAAAAGACTTTGATGATAATCTTAAGAGAGATTTATTGGAGTATATAGATACAAATGAAC
     ||  |            |   | |||| |   |  | | ||      |  |||    |  | |  |
   GAGTTCA-----------TCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAAGCTT
                    1290      1300      1310      1320      1330      X

     1150
   TATATTTACTTGATGAA


3. US-09-910-186A-31 (1-1233)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    45  Optimized Score  =    328  Significance = -1.15
Residue Identity  =   40%  Matches          =    367  Mismatches   =   501
Gaps              =    33  Conservative Substitutions              =     0

     350       360     X 370       380       390       400       410
   AATATAGAAAATCTACAACTAACGAATTCATTAAAT--GATGCTTTAAGAAATAATAATAAAGTCTATACTT
                       |  |  ||||  ||||   || |   ||     || ||||   ||   |
                       ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                       X       10        20        30        40        50

     420       430       440       450       460       470
   TTTTTTCTACAAACCTTGTTGAAAAAGCTAATACAGTTGTAGGTGCTTCACTTTTTGTAAAC-----TGGGT
   |   ||  | | ||     |   |  | |    | | |   ||||||  | ||   ||| ||      ||
   TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
      60        70        80        90       100       110       120

480       490       500       510       520       530       540       550
   AAAAGGAGTAATAGATGATTTTACATCTGA-ATCCACACAAAAAAGTACTATAGATAAAGTTTCAGATGTAT
   ||  | |  |  |||     ||  | ||||  ||  |    ||   ||  ||   |     |    ||
   AACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGA
    130       140       150       160       170       180       190

     560       570       580       590       600       610       620
   CCATAATTATTCCCTATATAGGACCTGCTTTGAATG-TAGGAAATGAAACAGCTAAAGAAAATTTTAAAAAT
    ||| ||  |   ||   ||   |  |  ||   || |      || | | |       ||||   | ||
   ACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACG
   200       210       220       230       240       250       260

     630       640       650       660       670       680       690
   GCTTTTGAAATAGGTGGAGCCGCTATCTTAATGGAGTTTATTCCAGAACTTATTGTACCTATAGTTGGATTT
    |  |    | |  |  | || | ||    |      | |   | | |   |   || || | ||||||
   ACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGA
  270       280       290       300       310       320       330       340

     700       710       720       730       740       750       760
   TTTACATTAGAATCATATGTAGGAAATAAAGGGCATATTATTATGACGATA--TCCAATGCTTTAAAGAAAA
   | | |||  |    |   |||  |  |  |         ||    ||| ||   ||||  || ||
   TCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCG
       350       360       370       380       390       400       410

     770       780       790       800       810       820       830
   GGGATCAAAAATGGACAGATATGTATGGTTTGATAGTATCGCAGTGGCTCTCAACGGTTAATACTCAATTTT
      |  | |   |   ||| || | ||  |  ||         ||   ||   ||  | |  | | |  |
   AATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGA
      420       430       440       450       460       470       480

    840       850       860                 870       880       890       900
   ATACAATAAAAGAAAGAATGTACAAT------GCTTTAAATAATCAATCACAAGCAATAGAAAAAATAATAG
   | |     |||      ||  ||  |      |  |  ||||   |     |||  ||     || | || |
   ACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCG
    490       500       510       520       530       540       550

     910       920       930       940       950       960       970
   AAGATCAATATAATAGATATAGTGAAGAAGATAAAATGAATATTAAC--ATTGATTTTAATGATATAGATTT
      |     | |  |  |  |     || | | | ||  ||  || |   || || |  |||| |||  | |
   CTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGATGAAATACTTCT
   560       570       580       590       600       610       620

      980       990      1000      1010      1020      1030      1040
   TAAACTTAATCAAAGTATAAATTTAGCAATAAACAATATAGATGATTTTATAAACCAATGTTCTATATCATA
     | ||| | ||  | |     | ||     || |    |||    |  |  | ||| | ||       |||
   CCATCTTCAACACCGAACTGTCTCAG--TCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATA
  630       640       650       660       670       680       690

    1050          1060      1070      1080         1090      1100
   TCTAATGAA----TAGAATGATTCCATTAGCTGTAAAAAAG--TTAAAAGACTTTGATGATAATCTTAAGAG
    || |   |    | |  | || |  | |  |  || ||||  |   |    ||  ||| |  |   ||||
   CCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGA-
  700       710       720       730       740       750       760

1110      1120      1130      1140      1150      1160      1170      1180
   AGATTTATTGGAGTATATAGATACAAATGAACTATATTTACTTGATGAAGTAAATATTCTAAAATCAAAAGT
   |   |||    |   |  ||| | |         |  | |  |  |||           || || || || |
   ACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACAACCAGAACT
  770       780       790       800       810       820       830       840

      1190            1200      1210      1220      1230  X
   AAATAGACACCTAAAA-----GACAGTATACCATTTGATCTTTCACTATATACCTAA
     | | ||| | |  |       | ||| | |  |  |   ||||  ||    |  |
   CTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAAATCTAACTCTCAGT
       850       860       870       880       890       900       910

   CCATC
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-31-inv.res made by bobryen on Thu 7 Nov 102 14:51:01-PST.

Query sequence being compared:US-09-910-186A-31' (1-1233)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-09-910-186A-31' (1-1233) with:
        File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                              *
N     -
C     -
E     -                                              *
S    0---------------------------------------------------------------------
      |  |   |      |      | |    |    | |      |      |   |  |     ||
SCORE 0  |   5      11    16 |   22    |27     33     38   | 44     49
STDEV   -5         -4       -3        -2       -1          0        1

                        PARAMETERS

Similarity matrix      Unitary    K-tuple                  4
Mismatch penalty             1    Joining penalty         30
Gap penalty               5.00    Window size            500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                        SEARCH STATISTICS

Scores:                 Mean       Median     Standard Deviation
                         44          37            7.51

Times:                  CPU                   Total Elapsed
                    00:00:00.00               00:00:00.00

Number of residues:               4027
Number of sequences searched:        3
Number of scores above cutoff:       3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                          Init. Opt.
Sequence Name      Description                    Length Score Score  Sig. Frame
---------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U   1338    49   446   0.67   0
   2. US-08-123-975A-1 Sequence 1, Application U   1338    49   446   0.67   0
                 ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U   1351    36   322  -1.07   0

1. US-09-910-186A-31' (1-1233)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =     49  Optimized Score  =    446  Significance =  0.67
Residue Identity  =    42%  Matches          =    522  Mismatches   =   640
Gaps              =     78  Conservative Substitutions             =     0

     20        30      X 40        50        60        70        80
   AGATCAAATGGTATACTGTCTTTTAGGTGTCTATTTACTTTTGATTTTAGAATATTTACTTCATCAAGTAAA
                        |  ||   |   |   ||  || | |      | | | | ||||||| | |
                       CTCGAGCCATGGCTCGTCTGCTG-TCTACCTTCACTGAATACATCAAGAACA
                       X       10        20         30        40        50

   90       100       110       120       130        140       150
   TATAGTTCATTTGTATCTATATACTCCAATAAATCTCTCTTAAGATTATC-ATCAAAGTCTTTTAACTTTTT
   |       |  |  |||   |  || |  ||    ||   | |  | ||| | |    ||  |   |||
   TCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCA
          60        70        80        90       100       110       120

 160       170       180       190       200       210       220       230
   TACAGCTAATGGAATCATTCTATTCATTAGATATGATATAGAACATTGGTTTATAAAATCATCTATATTGTT
    |      || |  ||      |   || |||  |||  | || | |    |   |  |  || || | |
   AAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGAT-CCAGCTGTTCAATCTGGAA
       130       140       150       160       170        180       190

         240       250       260       270       280       290       300
   TATTGCTAAATTTATACTTTGATTAAGTTTAAAATCTATATCATTAAAATCAATGTTAATATTCATTTTATC
   | || | ||||  |   | |  | |||    ||  ||||   ||  || || ||||        |    | |
   TCTTCCAAAATCGAAGTTATCCTGAAG----AATGCTATCGTATACAACTCTATGT--------ACGAAAAC
      200       210       220           230       240               250

       310       320       330       340       350       360       370
   TTCTTCACTATATCTATTATATTGATCTTCTATTATTTTTTCTATTGCTTGTGATTGATTATTTAAAGCATT
   |||| |||    |     ||    |||    | ||    ||| | | | | |   |||  | | ||  ||
   TTCTCCACCTCCTTCTGGATCCGTATCCCGAAATA---CTTCAACTCCATCTCTCTGAACAATGAATACA--
      260       270       280          290       300       310       320

     380       390       400       410          420       430        440
   GTACATTCTTTCTTTTATTGTATAAAATTGAGTATTAACCGT---TGAGAGCCACTGCGATACTATC-AAAC
      |||  |    |  || | | | ||||  |  |  |  ||   |  || | || | || |  |||   ||
   --CCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGAC
           330       340       350       360       370       380       390

       450       460       470       480       490       500       510
   CATACATATCTGTCCATTTTTGATCCCTTTTCTTTAAAGCATTGGATATCGTCATAATAATATGCCCTTTAT
     | ||   |  ||      | |  |    | ||  |  ||     | ||     |  || ||  |
   TCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTA
         400       410       420       430       440       450       460

     520       530       540       550       560       570            580
   TTCCTACATATGATTCTAATGTAAAAAATCCAACTATAGGTACAATAAGTTCTGGA-----ATAAACTCCAT
      | |    ||  |||    ||  |   ||||| || |    ||||| | |   |     || |||  |
   CATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCG
       470       480       490       500       510       520       530

        590       600       610       620       630       640       650
   TAAGATAGCGGCTCCACCTATTTCAAAAGCATTTTTAAAATTTTCTTTAGCTGTTTCATTTCCTACATTCAA
   |  ||| |       ||| || || ||    |   ||| ||   |  |     | | ||  | |    |  |
   TCTGATCGACCAGAAACCGATCTCCAA--TCTGGGTAACATCCACGCT-----TCTAATAACATCATGTTCA
     540       550       560         570       580            590       600

      660       670       680       690       700       710       720
   AGCAGGTCCTATATAGGGAATAATTATGGATACATCTGAAACTTTATCTATAGTACTTTTTTGTGTGGATTC
   | | || |   | | | | | | | |  | |||||||| | |     ||  | |   ||       | | |
    AACTGGACGGTTGTCGTG-ACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTG
           610        620       630       640       650       660       670

     730       740       750       760       770       780           790
    AGATGTAAAATCATCTATTACTCCTTTTACCCAGTTTACAAAAAGTGAAGCACCTACAACT----GTATTAG
    |     |||   ||| |  ||   |   ||      | |||     | | |    |  |||    |  | |
    AACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGAC
          680       690       700       710       720       730       740

       800       810       820       830       840       850       860
    CTTTTTCAACAAGGTTTGTAGAAAAAAAAGTATAGACTTTATTATTATTTCTTAAAGCATCATTTAATGAAT
        | ||  | |       | |  | | |   |  || ||  ||     |  | |   | |  | |  |||
    TACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAAT
        750       760       770       780       790       800       810

     870       880       890       900       910       920       930
    TCGTTAGTTGTAGATTTTCTATATTAGAAGGAAATGTTTGAGCATGTAAATATTCAAAAAGGCTATCT----
           |    | ||   | ||   ||| |    |  ||    ||| |  | |   ||   ||| ||
    GTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAAC
      820       830       840       850       860       870       880

                  940       950       960       970       980         990
    -----------CCATCCACAAAAATTTTTTTTAAAGCAGATTGTTTAATATACACAGG--GATATCTATGTC
               || |      |||||  |  | ||| |    |  |    ||   |||   |||||  |  |
    TCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGC
    890       900       910       920       930       940       950

       1000      1010      1020      1030      1040      1050      1060
    GTCAAAATTTGTAAATGGTTCTGTGTTTTCATTTGGTAAGTCTATGCCACTGCTTAAATCATTATCTAAAAT
      |||   | ||  ||   ||  |||| |  ||  | |     |   |  |      | || |   |   |
    AACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA-
  960       970       980       990      1000      1010      1020      1030

     1070      1080      1090      1100      1110      1120      1130
    CAACTGATCTATAGAAAAATTATTTTCTATAGTATTATTTTGTGTATTATATGCTATAGTTTCTGCTTTAGC
       ||| |   |||||||  | || |||    |   | |    |   |   |  | | || || | |
    -GGCTGGT--GTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCT-GTCTCAGGTAGTTG
             1040      1050      1060      1070      1080       1090

   1140      1150            1160      1170      1180      1190      1200
    TAAATCTTTTGAAAAACTA------TCTTTATTAGCTATGAAAAATAAATCCTCATTATTAACAATAATACA
    |||     |  || ||| |      | |   | |   ||| ||||| ||||  ||  |  ||||||  ||
    TAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGA-CAACAATGGTAAC
  1100      1110      1120      1130      1140      1150       1160

       1210      1220            1230  X
    CTGTTCAGATTTACCGGTAT------TTTTGGCCAT
        || | || | |||| |       ||   | ||
    GATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTC
 1170      1180      1190      1200    X 1210      1220

2. US-09-910-186A-31' (1-1233)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score      =     49  Optimized Score    =    446  Significance =  0.67
Residue Identity   =    42%  Matches            =    522  Mismatches   =   640
Gaps               =     78  Conservative Substitutions          =     0

      20        30      X 40        50        60        70        80
    AGATCAAATGGTATACTGTCTTTTAGGTGTCTATTTACTTTTGATTTTAGAATATTTACTTCATCAAGTAAA
                         |  ||   |   |   ||  ||  | |      | | | | ||||||| | |
                        CTCGAGCCATGGCTCGTCTGCTG-TCTACCTTCACTGAATACATCAAGAACA
                        X       10        20         30        40        50

    90       100       110       120       130        140       150
    TATAGTTCATTTGTATCTATATACTCCAATAAATCTCTCTTAAGATTATC-ATCAAAGTCTTTTAACTTTTT
    |       |  |  |||   |  || |  ||    ||   | |  | ||| | |    ||  |   |||
    TCATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCA
           60        70        80        90       100       110       120

  160       170       180       190       200       210       220       230
    TACAGCTAATGGAATCATTCTATTCATTAGATATGATATAGAACATTGGTTTATAAAATCATCTATATTGTT
     |      || |  ||      |   || |||  |||  | || | |    |   |  |  || || | |
    AAATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGAT-CCAGCTGTTCAATCTGGAA
        130       140       150       160       170        180       190

          240       250       260       270       280       290       300
    TATTGCTAAATTTATACTTTGATTAAGTTTAAAATCTATATCATTAAAATCAATGTTAATATTCATTTTATC
    | || | ||||  |   | |  | |||    ||  ||||   ||  || || ||||        |    | |
    TCTTCCAAAATCGAAGTTATCCTGAAG----AATGCTATCGTATACAACTCTATGT--------ACGAAAAC
       200       210       220           230       240               250

        310       320       330       340       350       360       370
    TTCTTCACTATATCTATTATATTGATCTTCTATTATTTTTTCTATTGCTTGTGATTGATTATTTAAAGCATT
    |||| |||    |     ||    |||    | ||    ||| | | | | |   |||  | | ||  ||
    TTCTCCACCTCCTTCTGGATCCGTATCCCGAAATA---CTTCAACTCCATCTCTCTGAACAATGAATACA--
       260       270       280          290       300       310       320

      380       390       400       410          420       430        440
    GTACATTCTTTCTTTTATTGTATAAAATTGAGTATTAACCGT---TGAGAGCCACTGCGATACTATC-AAAC
       |||  |    |  || | | | ||||  |  |  |  ||   |  || | || | || |  |||   ||
    --CCATCATCAACTGCATGGAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGAC
            330       340       350       360       370       380       390

        450       460       470       480       490       500       510
    CATACATATCTGTCCATTTTTGATCCCTTTTCTTTAAAGCATTGGATATCGTCATAATAATATGCCCTTTAT
      | ||   |  ||      | |  |    | ||  |  ||     | ||     |  || ||  |
    TCTGCAGGACACTCAGGAAATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTA
          400       410       420       430       440       450       460

      520       530       540       550       560       570            580
    TTCCTACATATGATTCTAATGTAAAAAATCCAACTATAGGTACAATAAGTTCTGGA-----ATAAACTCCAT
       | |    ||  |||    ||  |   ||||| || |    ||||| | |   |     || |||  |
    CATCAATCGCTGGATCTTCGTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCG
        470       480       490       500       510       520       530

         590       600       610       620       630       640       650
    TAAGATAGCGGCTCCACCTATTTCAAAAGCATTTTTAAAATTTTCTTTAGCTGTTTCATTTCCTACATTCAA
    |  ||| |       ||| || || ||    |   ||| ||   |  |     | | ||  | |    |  |
    TCTGATCGACCAGAAACCGATCTCCAA--TCTGGGTAACATCCACGCT-----TCTAATAACATCATGTTCA
      540       550       560         570       580            590       600

       660       670       680       690       700       710       720
    AGCAGGTCCTATATAGGGAATAATTATGGATACATCTGAAACTTTATCTATAGTACTTTTTTGTGTGGATTC
    | | || |   | | | | | | | |  | |||||||| | |     ||  | |   ||       | | |
    AACTGGACGGTTGTCGTG-ACACTCACCGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTG
           610        620       630       640       650       660       670

     730       740       750       760       770       780           790
    AGATGTAAAATCATCTATTACTCCTTTTACCCAGTTTACAAAAAGTGAAGCACCTACAACT----GTATTAG
    |     |||   ||| |  ||   |   ||      | |||     | | |    |  |||    |  | |
    AACGAAAAAGAAATCAAAGACCTGTACGACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGAC
          680       690       700       710       720       730       740

       800       810       820       830       840       850       860
    CTTTTTCAACAAGGTTTGTAGAAAAAAAAGTATAGACTTTATTATTATTTCTTAAAGCATCATTTAATGAAT
        | ||  | |       | |  | | |   |  || ||  ||     |  | |   | |  | |  |||
    TACCTGCAGTACGACAAACCGTACTACATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAAT
        750       760       770       780       790       800       810

     870       880       890       900       910       920       930
    TCGTTAGTTGTAGATTTTCTATATTAGAAGGAAATGTTTGAGCATGTAAATATTCAAAAAGGCTATCT----
           |    | ||   | ||   ||| |    |  ||    ||| |  | |   ||   ||| ||
    GTAGGTATCCGCGGTTACATGTACCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAAC
      820       830       840       850       860       870       880

                  940       950       960       970       980         990
    -----------CCATCCACAAAAATTTTTTTTAAAGCAGATTGTTTAATATACACAGG--GATATCTATGTC
               || |      |||||  |  | ||| |    |  |    ||   |||   |||||  |  |
    TCTTCCCTGTACCGTGGTACCAAATTCATCATCAAGAAATACGCGTCTGGTAACAAGGACAATATCGTTCGC
    890       900       910       920       930       940       950

       1000      1010      1020      1030      1040      1050      1060
    GTCAAAATTTGTAAATGGTTCTGTGTTTTCATTTGGTAAGTCTATGCCACTGCTTAAATCATTATCTAAAAT
      |||   | ||  ||   ||  |||| |  ||  | |     |   |  |      | || |   |   |
    AACAATGATCGTGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCA-
  960       970       980       990      1000      1010      1020      1030

     1070      1080      1090      1100      1110      1120      1130
    CAACTGATCTATAGAAAAATTATTTTCTATAGTATTATTTTGTGTATTATATGCTATAGTTTCTGCTTTAGC
       ||| |   |||||||  | || |||    |   | |    |   |   |  | | || || | |
    -GGCTGGT--GTAGAAAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCT-GTCTCAGGTAGTTG
             1040      1050      1060      1070      1080      1090

   1140      1150            1160      1170      1180      1190      1200
    TAAATCTTTTGAAAAACTA------TCTTTATTAGCTATGAAAAATAAATCCTCATTATTAACAATAATACA
    |||     |  || ||| |      | |   | |   ||| ||||| ||||  ||  |  ||||||  ||
    TAATGAAATCCAAGAACGACCAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGA-CAACAATGGTAAC
  1100      1110      1120      1130      1140      1150       1160

       1210      1220            1230  X
    CTGTTCAGATTTACCGGTAT------TTTTGGCCAT
        || | || | |||| |       ||   | ||
    GATATCGGTTTCATCGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTC
 1170      1180      1190      1200    X 1210      1220


3. US-09-910-186A-31’ (1-1233)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score    =       36  Optimized Score  =    322  Significance = -1.07
Residue Identity =      40%  Matches          =    385  Mismatches   =   492
Gaps             =       67  Conservative Substitutions              =     0

          310       320 X     330       340       350       360       370
    TCTTCTTCACTATATCTATTATATTGATCTTCTATTATTTTTTCTATTGCTTGTGATTGATTATTTAAAGCA
                        ||     ||  | | ||   || | |   | ||      || ||     ||
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X       10        20        30        40        50

        380       390       400       410                 420       430
    TTGTACATTCTTTCTTTTATTGTATAAAATTGAGTATTAAC--------CGTTGAGAGCCACTGCGATACT-
    |     |      |    ||   ||  |  ||  |  | ||         |||||     ||  || |  |
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90       100       110       120

      440       450       460             470       480       490       500
    -ATCAAACCATACATATCTGTCCATTTT----TGATCCCTTTTCTTTAAAGCATTGGATATCGTCATAATAA
     |   ||  | |   | | || ||   |    |  |||  |  || |||   ||  |   |  ||| ||| |
    AACTGAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAA--GATCCGTGTTACTCAGAATCA
       130       140       150       160       170         180       190

        510       520       530       540       550       560       570
    TATGCCCTTTATTTCCTACATATGATTCTAATGTAAAAAATCCAACTATAGGTACAATAAGTTCTGGAATAA
     |    | |  |   || | |||   |  | |        |||  ||  |     |     | | | ||||
    GAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTA-----TCCCGAAATAC
       200       210       220       230       240       250            260

      580       590       600       610       620       630       640
    ACTCCATTAAGATAGCGGCTCCACCTATTTCAAAAGCATTTTTAAAATTTTCTTTAGCTGTTTCATTTCCTA
    |       |  |   |||   |    ||| ||    || |    | |   || | | |||  | |      |
    A-------AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAA
                 270       280       290       300       310       320

    650       660       670       680       690       700       710
    CATTCAAAGCAGGTCCTATATAGGGAATAATTATGGATACATCTGAAACTTTATCTATAGTACTTTTTTGTG
    |  |    | | |  ||  ||  |   ||   |  |   |||||| |   | ||| |||      |     |
    CTCTGGTTGGAAGATCTCCATCCGCGGTA---ACCGTATCATCTGGACTCTGATCGATA------TCAACGG
     330       340       350          360       370       380

  720       730       740       750       760       770       780       790
    TGGATTCAGATGTAAAATCATCTATTACTCCTTTTACCCAGTTTACAAAAAGTGAAGCACCTACAACTGTAT
    |     || || |  | || || | |||  | |   ||  |   |||       |  || | |   |||  |
    TAAGACCAAATCTGTATTCTTCGAATACAACAT---CCGTGAAGACATCTCTGAATACATCAATCGCTGGTT
  390       400       410       420          430       440       450

          800       810       820       830       840       850       860
    TAGCTTTTTCAACAAGGTTTGTAGAAAAAAAAGTATAGACTTTATTATTATTTCTTAAAGCATCATTTAATG

       | ||  || ||    |      || ||   || |  ||  || |        ||||     || ||||
    CTTCGTTACCATCACCAATAACCTGAACAATGCTAAAATCTACATCA----ACGGTAAACTGGAATCTAATA
   460       470       480       490       500           510       520

        870       880       890       900       910       920       930
    AATTCGTTAGTTGTAGATTTTCTATATTAGAAGGAAATGTTTGAGCATGTAAATATTCAAAAAGGCTATC--
        | | |     | ||     |  |||     ||  ||   | ||| |  | | |  |    |  |||
    CCGACATCA--AAGACATCCGTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGA
     530         540       550       560       570       580       590

        940       950       960       970       980       990      1000
    TCCATCCACAAAAATTTTTTTTAAAGCAGATTGTTTAATATACACAGGGATATCTATGTCGTCAAAATTTGT
    ||   ||      || |   | |||      |   |  |  |||| |   | |||  |||  ||| ||
    TCGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTC--CAATATCGAA
     600       610       620       630       640       650         660

     1010          1020      1030      1040      1050            1060
    AAATGGTTC----TGTGTTTTCATTTGGTAAGTCTATGCCACTGCTTAAATCA-----TTATCTAAAATCAA
     || ||| |    |    | | | |  | |   ||     ||| ||    | |     | || || ||  ||
    GAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAA
     670       680       690       700       710       720       730

  1070       1080      1090      1100      1110      1120      1130
    CTGATCTATA-GAAAAATTATTTTCTATAGTATTATTTTGTGTATTATATGCTATAGTTTCTGCTT------
         ||||| |   |||  |  |    || | | ||   |  |    | |  | | | || | ||
    GAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAA
   740       750       760       770       780       790       800       810

       1140      1150      1160      1170      1180      1190      1200
    TAGCTAAATCTTTTGAAAAACTATCTTTATTAGCTATGAAAAATAAATCCTCATTATTAACAATAATACACT
       || | || ||  ||| || | |   | |    || | |   |   || |    |  |||    |  |
    ATCCTGACTCGTTCCAAATACAACCAGAACTCTAAAT-ACATCAACTACCGCGACCTGTACATCGGTGAAAA
           820       830       840        850       860       870       880

     1210      1220      1230  X
    GTTCAGATTTACCGGTATTTTTGGCCAT
    |||||   |     | |  | |  |  |
    GTTCATCATCCGTCGCAAATCTAACTCTCAGTCCATCAATGATGACAT
          890       900       910       920
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-32.res made by bobryen on Thu 7 Nov 102 14:38:02-PST.


Query sequence being compared:US-09-910-186A-32 (1-410)
Number of sequences searched:                    3
Number of scores above cutoff:                   3

      Results of the initial comparison of US-09-910-186A-32 (1-410) with:
        File : US08123975A.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -  **                                                          *
S    0---------------------------------------------------------------------
      |      |      |      |      |      |      |      |      |      |
SCORE 0     32     63     95    126    158    189    221    252    284
STDEV        0                                  1

                          PARAMETERS

Similarity matrix      PAM-150     K-tuple                  1
Threshold level of sim.    16%
Mismatch penalty             1     Joining penalty         20
Gap penalty               5.00     Window size            410
Gap size penalty          0.05
Cutoff score                 1
Randomization group          0

                        SEARCH STATISTICS

Scores:                 Mean        Median      Standard Deviation
                        106           15         154.18

Times:                 CPU                      Total Elapsed
                   00:00:00.00                  00:00:00.00

Number of residues:                  1704
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                             Init. Opt.
Sequence Name      Description                        Length Score Score  Sig. Frame
-------------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
  1. US-08-123-975A-2 Sequence 2, Application U    850   284   342   1.15    0
                    ****  0 standard deviation from mean ****
  2. US-08-123-975A-3 Sequence 3, Application U    415    20   189  -0.56    0
  3. US-08-123-975A-5 Sequence 5, Application U    439    14   132  -0.60    0


1. US-09-910-186A-32 (1-410)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score     =    284  Optimized Score  =    342  Significance =  1.15
Residue Identity  =    62%  Matches          =    252  Mismatches   =   125
Gaps              =      1  Conservative Substitutions              =    26

         x 10        20        30        40        50        60        70
   MAKNTGKSEQCIIVNNEDLFFIANKDSFSKDLAKAETIAYNTQNNTIENNFSIDQLILDNDLSSGIDLPNEN
             || | |||||||| | ||| ||:| | | |||| | ||| | |  |||| || | |:|| ||
         APGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSEN
         X       10        20        30        40        50        60

         80        90       100       110       120       130       140
   TEPFTNFDDIDIPVYIKQSALKKIFVDGDSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVYTFFSTNLV
   ||  | |  :|:||| || | |||| |    | || :||||  |    || | |||   |||| |||   :
   TESLTDF-NVDVPVYEKQPAIKKIFTDENTIFQYLYSQTFPLDIRDISLTSSFDDALLFSNKVYSFFSMDYI
     70        80        90       100       110       120       130

      150       160       170       180       190       200       210
   EKANTVVGASLFVNWVKGVIDDFTSESTQKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAI
     || || | ||  ||| :: ||  |:    | ||::|:| |:|||| |||||||||| || |||||:||:|
   KTANKVVEAGLFAGWVKQIVNDFVIEANKSNTMDKIADISLIVPYIGLALNVGNETAKGNFENAFEIAGASI
   140       150       160       170       180       190       200

    220       230       240       250       260       270       280
   LMEFIPELIVPIVGFFTLESYVGNKGHIIMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNA
   |:|||||| :|:|| | ||||: ||  || || ||| ||  || |||||||:||||||||||||||| || |
   LLEFIPELLIPVVGAFLLESYIDNKNKIIKTIDNALTKRNEKWSDMYGLIVAQWLSTVNTQFYTIKEGMYKA
 210       220       230       240       250       260       270       280

  290       300       310       320       330       340       350       360
   LNNQSQAIEKIIEDQYNRYSEEDKMNINIDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKK
   || |:|| | ||   || ||| :| |||||||||  |||  || || ||  ||| ||:|||| :|||||| |
   LNYQAQALEEIIKYRYNIYSEKEKSNINIDFNDINSKLNEGINQAIDNINNFINGCSVSYLMKKMIPLAVEK
         290       300       310       320       330       340       350

          370       380       390       400       410
   LKDFDDNLKRDLLEYIDTNELYLLDEVNILKSKVNRHLKDSIPFDLSLYT
   | |||  ||: || |||  | |||       |||||: ||   ||||| ||
   LLDFDNTLKKNLLNYIDENKLYLIGSAEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNI
       360       370       380       390       400  X    410       420


2. US-09-910-186A-32 (1-410)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score     =     20  Optimized Score  =    189  Significance = -0.56
Residue Identity  =    10%  Matches          =     44  Mismatches   =   333
Gaps              =      4  Conservative Substitutions              =    29

   X       10        20        30        40        50        60        70
   MAKNTGKSEQCIIVNNEDLFFIANKDSFSKDLAKAETIAYNTQNNTIENNFSIDQLILDNDLSSGIDLPNEN
           :              | |   |                  |      :      |  |  |
   RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYF
   X       10        20        30        40        50        60        70

         80        90       100       110       120       130       140
   TEPFTNFDDIDIPVYIKQSALKKIFVDGDSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVYTFFSTNLV
        | :   |      |: |     |:        |     :         | :   |  ::     |
   NSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRV-VFKYSQMINISDYINRWIFVTITNNRL
         80        90       100       110         120       130       140
       150       160       170       180       190       200       210
    EKANTVVGASLFVNWVKGVIDDFTSESTQKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAI
      :   : : |             :        |   |    |      |       ||          ::|
    NNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGI
        150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    LMEFIPELIVPIVGFFTLESYVGNKGHIIMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNA
    | :|  :       :: |  |  ||      : |   :         | :           :   |
    LKDFWGDYLQYDKPYYMLNLYDPNK---YVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKY
      220       230       240          250       260       270       280

   290       300       310       320       330       340       350       360
    LNNQSQAIEKIIEDQYNRYSEEDKMNINIDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKK
           | :  :  |       |                   | |  :                |    |
    ASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKM
       290       300       310       320       330       340       350

           370       380       390       400       410
    LKDFDDNLKRDLLEYIDTNELYLLDEVNILKSKVNRHLKDSIPFDLSLYT
                  :   |    |   |     : |  :
    NLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL
     360       370       380       390       400     X 410


3. US-09-910-186A-32 (1-410)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =      14  Optimized Score  =    132  Significance = -0.60
Residue Identity =     11%  Matches          =     32  Mismatches   =   239
Gaps             =       1  Conservative Substitutions              =    18

           110       120       130       140       150       160       170
    DSLFEYLHAQTFPSNIENLQLTNSLNDALRNNNKVYTFFSTNLVEKANTVVGASLFVNWVKGVIDDFTSEST
                              : | |      :   ||:: :        :          |   |
                        FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSS
                        X       10        20        30        40        50

         180       190       200       210       220       230       240
    QKSTIDKVSDVSIIIPYIGPALNVGNETAKENFKNAFEIGGAAILMEFIPELIVPIVGFFTLESYVGNKGHI
      | |       ||   :     |        :||             |  :                   |
    ANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLI
          60        70        80        90       100       110       120

       250       260       270       280       290       300       310
    IMTISNALKKRDQKWTDMYGLIVSQWLSTVNTQFYTIKERMYNALNNQSQAIEKIIEDQYNRYSEEDKMNIN
               :    :     :  |     |       : |      |    | | :         |:
    DINGKTKSVFFEYNIREDISEYINRWFFVTITNNLN-NAKIYINGKLESNTDIKDIREVIANGEIIFKLDGD
       130       140       150       160        170       180       190

     320       330       340       350       360       370       380
    IDFNDIDFKLNQSINLAINNIDDFINQCSISYLMNRMIPLAVKKLKDFDDNLKRDLLEYIDTNELYLLDEVN
    ||          ||               |      :       |    :              |     |
    IDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVG
      200       210       220       230       240       250       260

   390       400         X
    ILKSKVNRHLKDSIPFDLSLYT
        :              ||
    EILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIV
    270       280       290       300
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-33.res made by bobryen on Thu 7 Nov 102 14:51:25-PST.


Query sequence being compared:US-09-910-186A-33 (1-1314)
Number of sequences searched:                         3
Number of scores above cutoff:                        3

      Results of the initial comparison of US-09-910-186A-33 (1-1314) with:
        File : US08123975A.seq

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -                                                                 *
N     -
C     -
E     -                                                         *
S    0------------------------------------------------------------------------
       |      |      |    |  ||    ||   |  ||    ||   |   ||    ||  |   |
SCORE  0     62     124  |186|     248  |309|    371  |433|     495 | 557
STDEV                    -9  -8    -7   -6  -5   -4  -3   -2   -1   0

                               PARAMETERS

Similarity matrix       Unitary     K-tuple                    4
Mismatch penalty              1     Joining penalty           30
Gap penalty                5.00     Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                               SEARCH STATISTICS

Scores:                   Mean       Median     Standard Deviation
                           533          488       40.41

Times:                    CPU                   Total Elapsed
                      00:00:00.00               00:00:00.00

Number of residues:                    4027
Number of sequences searched:             3
Number of scores above cutoff:            3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                       Init. Opt.
Sequence Name     Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U  1338   557   788   0.59   0
   2. US-08-123-975A-1 Sequence 1, Application U  1338   557   788   0.59   0
                    **** 1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U  1351   487   678  -1.14   0


1. US-09-910-186A-33 (1-1314)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score     =    557  Optimized Score =    788  Significance =  0.59
Residue Identity =    61%  Matches         =    829  Mismatches   =   451
Gaps             =     71  Conservative Substitutions             =     0

            10        20        30        40           50        60
    GAATTCACGATGTCTTACACTAACGACAAAATCCTGATCCTGT---ACTTCAACAAACTGTACAAAAAAATC
                       ||   | ||     |   | ||||    |||||   ||     ||| || |||
                       CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATC
                       X       10        20        30        40        50

   70        80        90       100       110       120       130       140
    AAAGACAACTCTATCCTGGACATGCGTTACGAAAACAACAAATTCATCGACATCTCTGGCTATGGTTCTAAC
    |   | | ||| |||||| || |||| ||||||  |||  |  | |||||| | ||| |||| | ||| ||
    ATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAA
         60        70        80        90       100       110       120

          150       160       170       180       190       200       210
    ATCTCTATCAACGGTGACGTCTACATCTACTCTACTAACCGCAACCAGTTCGGTATCTACTCTTCTAAACCG
    |||   |||     | | ||  || || |  | |   ||   || ||| ||    | | |  |    || |
    ATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCT
      130       140       150       160       170       180       190

        220       230       240       250       260       270       280
    TCTGAAGTAAACATCGCTCAGAACAACGACATCATCTACAACGGTCGTTACCAGAACTTCTCTATCTCTTTC
    ||  || |  |  |    | ||| || |  ||| | ||||||  |   ||| | |||||||| | ||| |||
    TCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTC
    200       210       220       230       240       250       260

      290       300       310       320       330       340       350
    TGGGTTCGTATCCCGAAATACTTCAACAAAGTTAACCTGAACAACGAATACACTATCATCGACTGCATCCGT
    ||| | |||||||||||||||||||||    |    |||||||| |||||||| |||||| |||||||
    TGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCAT---G
  270       280       290       300       310       320       330

    360       370       380       390       400       410       420
    AACAACAACTCTGGTTGGAAAATCTCTCTGAACTACAACAAAATCATCTGGACTCTGCAGGACACTGCTGGT
     | ||||| |||||||||||| | ||||||||||||    ||||||||||||||||||||||||||   |
    GAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAA
   340       350       360       370       380       390       400       410

  430       440       450       460       470       480       490       500
    AACAACCAGAAACTGGTTTTCAACTACACTCAGATGATCTCTATCTCTGACTACATTAATAAATGGATCTTC
    | ||| |||    | || ||||| ||| |||||||||||   |||||||||||||| |||   |||||||||
    ATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTC
           420       430       440       450       460       470       480

          510       520       530       540       550       560       570
    GTTACTATCACTAACAACCGTCTGGGTAACTCTCGTATCTACATCAACGGTAACCTGATCGATGAAAAATCT
    ||||| ||||| ||||| ||||||  ||||||    ||||||||||||||    ||||||||  | ||| |
    GTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCG
         490       500       510       520       530       540       550

        580       590       600       610       620       630       640
    ATCTCTAACCTGGGTGACATCCACGTTTCTGACAACATCCTGTTCAAAATCGTTGGTTGCAACGACAC---G
    ||||| || |||||| ||||||||| |||| | |||||| |||||||| | |  |||||    |||||
    ATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCAC
       560       570       580       590       600       610       620

         650       660       670       680       690       700       710
    CGTTACGTTGGTATCCGTTACTTCAAAGTTTTCGACACTGAACTGGGTAAAACTGAAATCGAAACTCTGTAC
    || ||| |  | |||   ||||||||  | |||||||  ||||||    |||  |||||| ||   ||||||
    CGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTAC
     630       640       650       660       670       680       690

       720       730       740       750       760       770       780
    TCTGACGAACCGGACCCGTCTATCCTGAAAGACTTCTGGGGTAACTACCTGCTGTACAACAAACGTTACTAC
        || |  |  |  |   |||||||||||||||||||||| ||||||||| |||| ||||||  ||||||
    GACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTAC
   700       710       720       730       740       750       760       770

     790       800       810         820       830                 840
    CTGCTGAACCTGCTCCGGACTGACAAAT--CTATCACTCAGAACTCTAACT----------TCCTGAACATC
     ||||||| |||  |    |  ||||||   |     |||  | | ||  |           | || || |
    ATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTG
           780       790       800       810       820       830       840

     850       860       870       880       890       900       910
    AACCAGCAGCGTGGTGTTTATCAGAAACCTAATATCTTCTCTAACACTCGTCTGTACACTGGTGTTGAAGTT
    ||    | |||||||  |  |  ||   | || |||| |   ||| ||   ||||||  ||||    || |
    AAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTC
         850       860       870       880       890       900       910

   920       930       940       950       960       970       980       990
    ATCATCCGTAAAAACGGTTCTACTGACATCTCTAACACTGACAACTTCGTACGTAAAAACGACCTGGCTTAC
    ||||||   ||| |||  |||           |||||  |||||  |||| || || || || |  |  |||
    ATCATCAAGAAATACGCGTCT---------GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATAC
       920       930                940       950       960       970

          1000      1010      1020      1030      1040      1050      1060
    ATCAACGTTGTTGACCGTGACGTTGAATACCGTCTGTACGCTGACATCTCTATCGCTAAACCGGAAAAAATC
    ||||| ||||| |      ||   ||||||||||||    |  |    |||   |||      ||||| |||
    ATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATC
    980       990      1000      1010      1020      1030      1040

        1070      1080      1090      1100      1110      1120
    ATCAAACTGATCCGTACTTCTAACTCTAACAACTCTCTGGGTCAGATCATCGTTATGGACTC----------
     |        |    |   |  ||  |   ||   ||||  |||| |  | || ||| | ||
    TTGTCTGCTCTGGAAATCCCGGACGTTGGTAA---TCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGAC
 1050      1060      1070      1080         1090      1100      1110

           1130      1140      1150      1160      1170      1180      1190
    -----GATCGGTAACAACTGCACTATGAACTTCCAGAACAACAACGGTGGTAACATCGGTCTGCTGGGTTTC
          |||  |||||| ||||  |||||  | ||| ||||||| |||    | |||||| |  | ||||||
    CAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTC
  1120      1130      1140      1150      1160      1170      1180      1190

         1200                  1210      1220      1230      1240      1250
    CACTCTAACAAC------------CTGGTTGCTTCTTCATGGTACTACAACAACATCCGTAAAAACACTTCT
    |||     ||||            |||||||||||    |||||| |     | |||        | ||
    CACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGC
          1200      1210      1220      1230      1240      1250      1260

         1260      1270      1280      1290      1300                 1310
    TCTAACGGTTGCTTCTGGTCTTTCATCTCTAAAGAACACGGTTGGCAGGA-----------AAACTAAGAAT
     ||   |||||||  |||   |||||| |    ||  ||||||||   ||           || |   |||
    ACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAA
        1270      1280      1290      1300      1310      1320      1330

     X
    TC
     |
    GCTT
     X


2. US-09-910-186A-33 (1-1314)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score      =    557  Optimized Score =     788  Significance =  0.59
Residue Identity   =    61%  Matches         =     829  Mismatches   =   451
Gaps               =     71  Conservative Substitutions              =     0

            10        20        30        40           50        60
    GAATTCACGATGTCTTACACTAACGACAAAATCCTGATCCTGT---ACTTCAACAAACTGTACAAAAAAATC
                       ||   | ||     |   | ||||    |||||   ||     ||| || |||
                       CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATC
                       X       10        20        30        40        50

   70        80        90       100       110       120       130       140
    AAAGACAACTCTATCCTGGACATGCGTTACGAAAACAACAAATTCATCGACATCTCTGGCTATGGTTCTAAC
    |   | | ||| |||||| || |||| ||||||  |||  |  | |||||| | ||| |||| | ||| ||
    ATCAATACCTCCATCCTGAACCTGCGCTACGAATCCAATCACCTGATCGACCTGTCTCGCTACGCTTCCAAA
         60        70        80        90       100       110       120

          150       160       170       180       190       200       210
    ATCTCTATCAACGGTGACGTCTACATCTACTCTACTAACCGCAACCAGTTCGGTATCTACTCTTCTAAACCG
    |||   |||     | | ||  || |  |  |     |    || ||| ||    | | |  |    || |
    ATCAACATCGGTTCTAAAGTTAACTTCGATCCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCT
      130       140       150       160       170       180       190

        220       230       240       250       260       270       280
    TCTGAAGTAAACATCGCTCAGAACAACGACATCATCTACAACGGTCGTTACCAGAACTTCTCTATCTCTTTC
    ||  || |  |  |    | ||| || |  ||| | ||||||  |   |||   |||||||| |  || |||
    TCCAAAATCGAAGTTATCCTGAAGAATGCTATCGTATACAACTCTATGTACGAAAACTTCTCCACCTCCTTC
    200       210       220       230       240       250       260

      290       300       310       320       330       340       350
    TGGGTTCGTATCCCGAAATACTTCAACAAAGTTAACCTGAACAACGAATACACTATCATCGACTGCATCCGT
    ||| | |||||||||||||||||||||    |    |||||||| |||||||| |||||| |||||||
    TGGATCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCAT---G
  270       280       290       300       310       320       330

    360       370       380       390       400       410       420
    AACAACAACTCTGGTTGGAAAATCTCTCTGAACTACAACAAAATCATCTGGACTCTGCAGGACACTGCTGGT
     | ||||| |||||||||||| | ||||||||||||    ||||||||||||||||||||||||||   |
    GAAAACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAA
   340       350       360       370       380       390       400       410

  430       440       450       460       470       480       490       500
    AACAACCAGAAACTGGTTTTCAACTACACTCAGATGATCTCTATCTCTGACTACATTAATAAATGGATCTTC
    | ||| |||    | || ||||| ||| |||||||||||   |||||||||||||| |||   |||||||||
    ATCAAACAGCGTGTTGTATTCAAATACTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTC
           420       430       440       450       460       470       480

          510       520       530       540       550       560       570
    GTTACTATCACTAACAACCGTCTGGGTAACTCTCGTATCTACATCAACGGTAACCTGATCGATGAAAAATCT
    ||||| ||||| ||||| ||||||  ||||||    ||||||||||||||    ||||||||  | ||| |
    GTTACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCG
         490       500       510       520       530       540       550

        580       590       600       610       620       630       640
    ATCTCTAACCTGGGTGACATCCACGTTTCTGACAACATCCTGTTCAAAATCGTTGGTTGCAACGACAC---G
    ||||| || |||||| ||||||||| |||| | |||||| |||||||| | |  |||||    |||||
    ATCTCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCAC
       560       570       580       590       600       610       620

         650       660       670       680       690       700       710
    CGTTACGTTGGTATCCGTTACTTCAAAGTTTTCGACACTGAACTGGGTAAAACTGAAATCGAAACTCTGTAC
    || ||| |  | |||   ||||||||  | |||||||  ||||||    |||  |||||| ||    |||||
    CGCTACATCTGGATCAAATACTTCAATCTGTTCGACAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTAC
     630       640       650       660       670       680       690

       720       730       740       750       760       770       780
    TCTGACGAACCGGACCCGTCTATCCTGAAAGACTTCTGGGGTAACTACCTGCTGTACAACAAACGTTACTAC
        || |  |  |  |   |||||||||||||||||||||| ||||||||| |||| ||||||  ||||||
    GACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTAC
   700       710       720       730       740       750       760       770

     790       800       810         820       830                 840
    CTGCTGAACCTGCTCCGGACTGACAAAT--CTATCACTCAGAACTCTAACT----------TCCTGAACATC
     ||||||| |||  |    |  ||||||   |     |||  | | ||  |           | || || |
    ATGCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTACCTG
           780       790       800       810       820       830       840

     850       860       870       880       890       900       910
    AACCAGCAGCGTGGTGTTTATCAGAAACCTAATATCTTCTCTAACACTCGTCTGTACACTGGTGTTGAAGTT
    ||    | |||||||  |  |  ||   | || |||| |   ||| ||   ||||||  ||||    || |
    AAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTACCAAATTC
          850       860       870       880       890       900       910

   920       930       940       950       960       970       980       990
    ATCATCCGTAAAAACGGTTCTACTGACATCTCTAACACTGACAACTTCGTACGTAAAAACGACCTGGCTTAC
    ||||||   ||| |||  |||           |||||  |||||  |||| || || || || |  |  |||
    ATCATCAAGAAATACGCGTCT---------GGTAACAAGGACAATATCGTTCGCAACAATGATCGTGTATAC
       920       930                 940       950       960       970

           1000      1010      1020      1030      1040      1050      1060
    ATCAACGTTGTTGACCGTGACGTTGAATACCGTCTGTACGCTGACATCTCTATCGCTAAACCGGAAAAAATC
    ||||| ||||| |      ||   ||||||||||||    |  |    |||   |||      ||||| |||
    ATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGAAAAGATC
     980       990      1000      1010      1020      1030      1040

        1070      1080      1090      1100      1110      1120
    ATCAAACTGATCCGTACTTCTAACTCTAACAACTCTCTGGGTCAGATCATCGTTATGGACTC----------
     |        |    |   |  ||  |   ||   ||||  |||| |  | || ||| | ||
    TTGTCTGCTCTGGAAATCCCGGACGTTGGTAA---TCTGTCTCAGGTAGTTGTAATGAAATCCAAGAACGAC
 1050      1060      1070      1080         1090      1100      1110

           1130      1140      1150      1160      1170      1180      1190
    -----GATCGGTAACAACTGCACTATGAACTTCCAGAACAACAACGGTGGTAACATCGGTCTGCTGGGTTTC
          |||  |||||| ||||  |||||  | ||| ||||||| |||      | ||||||  |  | ||||||
    CAGGGTATCACTAACAAATGCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCATCGGTTTC
  1120      1130      1140      1150      1160      1170      1180      1190

         1200                  1210      1220      1230      1240      1250
    CACTCTAACAAC------------CTGGTTGCTTCTTCATGGTACTACAACAACATCCGTAAAAACACTTCT
    |||     ||||                ||||||||||||    |||||| |     | |||       | ||
    CACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTCCTCTCGC
          1200      1210      1220      1230      1240      1250      1260

         1260      1270      1280      1290      1300                 1310
    TCTAACGGTTGCTTCTGGTCTTTCATCTCTAAAGAACACGGTTGGCAGGA-----------AAACTAAGAAT
     ||   |||||||  |||   |||||| |    ||  ||||||||   ||            || |   |||
    ACTCTGGGTTGCTCTTGGGAGTTCATCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAACCCGGGAAA
        1270      1280      1290      1300      1310      1320      1330

      X
     TC
      |
     GCTT
      X

3. US-09-910-186A-33 (1-1314)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =    487  Optimized Score    =    678  Significance = -1.14
Residue Identity =    54%  Matches            =    740  Mismatches   =   520
Gaps              =     90  Conservative Substitutions              =     0

   20        30        40        50        60        70        80        90
    CTAACGACAAAATCCTGATCCTGTACTTCAACAAACTGTACAAAAAAATCAAAGACAACTCTATCCTGGACA
                         ||   ||||||||||    |     |||||    ||||    |||||| ||
                        ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACC
                        X        10        20        30        40        50

           100       110       120       130       140       150       160
    TGCGTTACGAAAACAACAAATTCATCGACATCTCTGGCTATGGTTCTAACATCTCTATCAACGGTGACGTCT
    |||||||| || |||||||  | |||||  | ||||| || ||| |||| |     |  |||  |  ||
    TGCGTTACAAAGACAACAATCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTG
          60        70        80        90       100       110       120

        170       180       190       200       210       220       230
    ACATCTACTCTACTAACCGCAACCAGTTCGGTATCTACTCTTCTAAACCGTCTGAAGTAAACATCGCTCAGA
    |  |        | | ||   |||||||||    |   ||||||       ||| |  |     |  ||||||
    AACT------GAATGACAAGAACCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGA
             130       140       150       160       170       180       190

      240       250       260       270       280       290       300
    ACAACGACATCATCTACAACGGTCGTTACCAGAACTTCTCTATCTCTTTCTGGGTTCGTATCCCGAAATACT
    |  |  |||||||| ||||      | || | ||||||||| | || |||||| | |||||||||||||||
    ATCAGAACATCATCTTCAACTCCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACA
           200       210       220       230       240       250       260

   310       320                 330       340       350       360       370
    TCAACAAAGTTAACCTGA---------ACAACGAATACACTATCATCGACTGCATCCGTAACAACAACTCTG
      ||| | | || || ||       |||| |||||||| |||||| |||||||    || || |||||||
    AGAACGACGGTATCCAGAATTACATCCACAATGAATACACCATCATCAACTGCAT---GAAGAATAACTCTG
         270       280       290       300       310          320       330

           380       390       400       410       420       430       440
    GTTGGAAAATCTCTCTGAACTACAACAAAATCATCTGGACTCTGCAGGACACTGCTGGTAACAACCAGAAAC
    ||||||| ||||||  |   |   |||   |||||||||||||||   || |     ||||| | | |
    GTTGGAAGATCTCCATCCGCGGTAACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTG
          340       350       360       370       380       390       400

         450       460       470       480       490       500       510
    TGGTTTTCAACTACACTCAGATGATCTCTATCTCTGACTACATTAATAAATGGATCTTCGTTACTATCACTA
    |  | || |  ||||              ||||||||| ||||| |||   ||| |||||||||| ||||| |
    TATTCTTCGAATACAACATCCGTGAAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCA
        410       420       430       440       450       460       470

       520       530       540       550       560       570       580
    ACAACCGTCTGGGTAACTCTCGTATCTACATCAACGGTAACCTGATCGATGAAAAATCTATCTCTAACCTGG
    | |||   |||   ||  ||   |||||||||||||||||| |||     | | |     |||    || |
    ATAAC---CTGAACAATGCTAAAATCTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCC
      480          490       500       510       520       530       540

     590       600       610       620       630          640       650
    GTGACATCCACGTTTCTGACAACATCCTGTTCAAAATCGTTGGTTGCAACGA---CACGCGTTACGTTGGTA
    ||||  |   || |   |   | ||| | ||||| | |  |||  || ||    || |  | | |  |  |
    GTGAAGTTATCGCTAACGGTGAAATCATCTTCAAACTGGACGGTGACATCGATCGTACCCAGTTCATCTGGA
       550       560       570       580       590       600       610

      660       670       680       690       700       710       720
    TCCGTTACTTCAAAGTTTTCGACACTGAACTGGGTAAAACTGAAATCGAAACTCTGTACTCTGACGAACCGG
    |    ||||||    | ||| |||| ||||||  | |  |  | ||||||   | ||||     | |  |
    TGAAATACTTCTCCATCTTCAACACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTT
     620       630       640       650       660       670       680

    730       740       750       760       770       780       790
    ACCCGTCTATCCTGAAAGACTTCTGGGGTAACTACCTGCTGTACAACAAACGTTACTACCTGCTGAACCTGC
    || |      |||||||||||||||||||||    ||| ||||||||||   |||||  || | ||
    ACTCCGAATACCTGAAAGACTTCTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTG
   690       700       710       720       730       740       750       760

 800        810       820       830        840         850       860
    TCCGGACTGACAAATCTATCACTCAGAACTCTAACT-TCCTGAACATCAA--CCAGCAGCGTGGTGTTT---
         |   ||   |  ||||  | |||     ||| |||  |    | ||  || |   |||      |
    GTAACAAGAACTCTTACATCAAACTGAAGAAAGACTCTCCGGTTGGTGAAATCCTGACTCGTTCCAAATACA
           770       780       790       800       810       820        830

      870       880       890       900       910       920       930
    ATCAGAAACCTAATATCTTCTCTAACACTCGTCTGTACACTGGTGTTGAAGTTATCATCCGTAAAAACGGTT
    | |||||  |||| | | ||    ||      ||||||| ||||   | | |||||||||||   ||     |
    ACCAGAACTCTAAATACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGTCGCAA---AT
         840       850       860       870       880       890         900

    940       950       960       970       980       990      1000
    CTACTGACATCTCTAACACTGACAACTTCGTACGTAAAAACGACCTGGCTTACATCAACGTTGTTGACCGTG
    |||         || | || |||  || |||||||||||| |  |||      ||| |  || |  ||| 
    CTAACTCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGA
          910       920       930       940       950       960       970

 1010      1020      1030      1040      1050      1060      1070      1080
    ACGTTGAATACCGTCTGTACGCTGACATCTCTATCGCTAAACCGGAAAAAATCATCAAACTGATCCGTACTT
    |    ||||  ||| | ||| |  |||  |   ||   ||   ||| ||||   |    |||   |  |  |
    ATCAGGAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCT
        980       990      1000      1010      1020      1030      1040

         1090      1100      1110      1120      1130         1140      1150
    CTAACTCTAAC-AACTCTCTGGGTCAGATCATCGTTATGGACTCGATCGGTAACAACTGCACTATGAACT
    || | ||  || ||||||      |    ||     | | |  |||     | |  | || | ||    |
   CTGATTCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGC
    1050      1060      1070      1080      1090      1100      1110

         1160                  1170      1180      1190          1200
   TCCAGAACAACAACG------------GTGGTAACATCGGTCTGCTGGGTTTCCAC----TCTAACAACCTG
   | | |  ||| || |             ||   | ||||||||| | ||| |||||    ||||  || |||
   TGCTGTTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTG
  1120      1130      1140      1150      1160      1170      1180

   1210        1220      1230                                 1240
   GTTGCTTCTTC--ATGGTACTACAACAACATCCG---------------------------TAAAAACACTT
   ||  | | |||  |   ||| |  || || || |                           ||||  ||
   GTATCGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAAC
1190      1200      1210      1220      1230      1240      1250      1260

1250               1260      1270      1280      1290      1300      1310
   CTTCTAAC---------GGTTGCTTCTGGTCTTTCATCTCTAAAGAACACGGTTGGCAGGAAAACTAAGAAT
   | |  |||         ||||||   |||   |||||| | |||||  | ||||||   ||| | |||
   CGTACAACCTGAAACTGGGTTGCAATTGGCAGTTCATCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTC
        1270      1280      1290      1300      1310      1320      1330

    X
   TC
   |
   TAGAGTCGAGGCCTGCAG
    X 1340      1350
```

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-33-inv.res made by bobryen on Thu 7 Nov 102 14:51:42-PST.


Query sequence being compared:US-09-910-186A-33' (1-1314)
Number of sequences searched:                     3
Number of scores above cutoff:                    3

      Results of the initial comparison of US-09-910-186A-33' (1-1314) with:
        File : US08123975A.seq
```

Complement

```
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -                                                     .
U     -
E     -                                                                *
N     -
C     -
E     -                                                    *
S    0----------------------------------------------------------------------
       ||     |  |   | |    ||     | |    |      ||     |      ||      |
SCORE 0 |     4  |   7 |  11|     15 |   18     22|    26     29|    33
STDEV  -8      -7    -6    -5       -4   -3      -2    -1       0


                          PARAMETERS

Similarity matrix       Unitary      K-tuple                    4
Mismatch penalty              1      Joining penalty           30
Gap penalty                5.00      Window size              500
Gap size penalty           0.33
Cutoff score                  1
Randomization group           0

                        SEARCH STATISTICS

Scores:                 Mean      Median     Standard Deviation
                         31         28           3.46

Times:                  CPU                  Total Elapsed
                   00:00:00.00               00:00:00.00

Number of residues:                  4027
Number of sequences searched:           3
Number of scores above cutoff:          3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                              Init.  Opt.
Sequence Name     Description                       Length Score Score   Sig. Frame
-----------------------------------------------------------------------------------
   1. US-08-123-975A-4 Sequence 4, Application U     1338     33   462   0.58    0
   2. US-08-123-975A-1 Sequence 1, Application U     1338     33   462   0.58    0
                    ****  1 standard deviation below mean ****
   3. US-08-123-975A-6 Sequence 6, Application U     1351     27   458  -1.15    0


1. US-09-910-186A-33' (1-1314)
   US-08-123-975A-4 Sequence 4, Application US/08123975A

Initial Score      =      33  Optimized Score  =    462  Significance =  0.58
Residue Identity   =     41%  Matches          =    560  Mismatches   =   711
Gaps               =      91  Conservative Substitutions             =     0

        X       10        20        30        40        50        60
        GAATTCTTAGTTTTCCTGCCAACCGTGTTCTTTAGAGATGAAAGACCAGAAGCAACCGTTAGAAGA
          ||   | || | |   | | |     |   || |     || | ||  |  | |        ||
  CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
        X 10        20        30        40        50        60        70

    70        80        90       100       110       120       130
  AGTGTTTTTACGGATGTTGTTGTAGTACCATGAAGAAGCAACCAGGTTGTTAGAGTGGAAACCCAGCA----
  |       |||| |      |  | |  | |||   | |   |  |   |  |  |  |||  || ||
  ACCTGCGCTACGAA------TCCAATCACCTGATCGACCTGTCTCG--CTACGCTTCCAAAATCAACATCGG
        80              90       100       110         120       130

     140       150       160       170       180       190       200
  GACCGATGTTACCACCGTTGTTGTTCTGGAAGTTCATAGTGCAGTTGTTACCGATCGAGTCCATAACGAT-G
    |  | |||| |  || |   | ||   |||       | ||| ||||     | || ||    |  || |
  TTCTAAAGTTAACTTCGAT-CCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCG
   140       150        160       170       180       190       200

    210       220       230       240       250       260       270
  ATCTGACCCAGAGAGTTGTTAGAGTTAGAAGTACGGATCAGTTTGATGATTTTTTCCGGTTTAGCGATAGAG
  |  | | || ||    || || ||   |   |    |  ||  ||  | || | |   |    |   |
  AAGTTATCCTGAAGAATGCTATCGT---ATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGA---
  210       220       230          240       250       260       270

  280       290       300       310       320       330       340
  ATGTCAGCGTACAGACGGTATTCAACGTCACGGTCAACAACGTTGATGTAAGCCAGGTCGTTTTTACGTACG
     || |  | | ||     ||||||  ||        |||  |||    | |    ||   |  | | |
  ---TCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAA
         280       290       300       310       320       330       340

350        360       370       380       390       400          410
  A-AGTTGTCAGTGTTAGAGATGTCAGTAGAACCGTTTTTACGGATGATAACTTCAACAC---CAGTGTACAG
  | | || |   ||  |   || || | |  || ||     |   ||    || ||  ||   |||   |
  ACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCA
       350       360       370       380       390       400       410

  420       430       440       450        460        470       480
  ACGAGTGTTAGAGAAGATATTAGGTTTCTGATAAACACCA-CGCTG-CTGGTTGATGTTCAGGAAGTTAGAG
  |  || ||     |    | ||  | || ||| | || || | ||| ||   | |    | |||  || |
  AACAGCGTGTTGTATTCAAATA-CTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
     420       430        440       450       460       470       480

  490       500       510       520       530       540           550
  TTCTGAGTGATAGATTTGTCAGTCCGGAGCAGGTTCAGCAGGTAGTAACGTTTGTTGTAC----AGCAGGTA
    |      |   ||              ||   ||  ||   |    ||| || |  ||    | | | |
  ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
    490       500       510       520       530       540       550

    560       570       580       590       600       610       620
  GTTACCCCAGAAGTCTTTCAGGATAGACGGGTCCGGTTCGTCAGAGTACAGAGTTTCGATTTCAGTTTTACC
     |  |  |    | | || | |        |    |  ||| | |  |  |||    |  || |     |
  TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
  560       570       580       590       600       610       620

  630       640       650       660       670       680       690
  CAGTTCAGTGTCGAAAACTTTGAAGTAACGGATACCAACGTAACGCGTGTCGTTGCAACCAACGATTT----
   |  || |  || || ||||  |  |    ||   ||| | |  |   |     | || ||| ||  |
      TACATCTGGATCAAATACTTCAATCTGTTCGA---CAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTAC
    630       640       650       660          670       680       690

          700       710       720       730       740       750       760
      --TGAACAGGATGTTGTCAGAAACGTGGATGTCACCCAGGTTAGAGATAGATTTTTCATCGATCAGGTTACC
          | |||     |    | | | || | | |  |  || |    |       | |  | | | |     |
      GACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTAC
     700       710       720       730       740       750       760       770

        770       780       790       800       810         820       830
      GTTGATGTAGATACGAGAGTTACCCAGACGGTTGTTAGTGATAGTAACGAAG--ATCCATTTATTAATGTAG
       |     |  ||  |   | | |  | |     |||   |  |  || | ||  ||||     |  |||||
      AT---GCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTA-
                780       790       800       810       820       830

        840       850       860         870       880       890       900
      TCAGAGATAGAGATCATCTGAGTGTAGT--TGAAAACCAGTTTCTGGTTGTTACCAGCAGTGTCCTGCAGAG
              | || ||  |   ||   ||  |||  ||||   |||   ||    |  |  ||| | |  |
      ----CCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTA
         840       850       860       870       880       890       900

        910       920       930       940       950       960       970
      TCCAGATGATTTTGTTGTAGTTCAGAGAGATTTTCCAACCAGAGTTGTTGTTACGGATGCAGTCGATGATAG
       | |  | ||  |   | |    | |    | |   ||| ||    |    ||  | |     | ||||| |
      CCAAATTCATCATCAAGAA----ATACGCGTCTGGTAACAAG----GACAATATCGTTCGCAACAATGATCG
       910       920           930       940           950       960       970

      980          990      1000      1010      1020           1030      1040
      TGTAT---TCGTTGTTCAGGTTAACTTTGTTGAAGTATTTCGGGATACGAA-----CCCAGAAAGAGATAGA
      |||||   ||  ||||   |||||       |||     || || ||| ||     | |||   |   ||||
      TGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGA
             980       990      1000      1010      1020      1030      1040

           1050       1060      1070      1080      1090      1100      1110
      GAAGTTCTGGT-AACGACCGTTGTAGATGATGTCGTTGTTCTGAGCGATGTTTACTTCAGACGGTTTAGAAG
       ||| ||| ||   |    |   |    || || | |  ||||    | |  || ||   | |   |  |||
      AAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGG--TAGTTGTAATGAAATCCAAG
          1050      1060      1070      1080      1090        1100      1110

          1120      1130      1140      1150      1160      1170      1180
      AGTAGATACCGAACTGGTTGCGGTTAGTAGAGTAGATGTAGACGTCACCGTTGATAGAGATGTTAGAACCAT
      |      |  | |    |  |   | | | | |  || |  | | || |  || ||  ||| |  |   |||
      AACGACCAGGGTATCACTAACAAAT-GCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCAT
          1120      1130       1140      1150      1160      1170      1180

                    1190      1200      1210        1220      1230      1240
      AG------------CCAGAGATGTCGATGAATTTGTTGTTTTC--GTAACGCATGTCCAGGATAGAGTTGTC
       |             ||   || ||| | || | |||| || |   |    ||       ||| ||    ||
      CGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTC
         1190      1200      1210      1220      1230      1240      1250

          1250      1260      1270      1280      1290      1300      1310   X
      TTTGATTTTTTTGTACAGTTTGTTGAAGTACAGGATCAGGATTTTGTCGTTAGTGTAAGACATCGTGAATTC
       |       | ||    | |  | | ||| ||    | || |  || || | | |    || ||     |
      CTCTCGCACTCTGGGTTGCTCTTGGGAGTTCA--TCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
       1260      1270      1280        1290      1300      1310      1320    X

      CCCGGGAAAGCTT
       1330


2. US-09-910-186A-33' (1-1314)
   US-08-123-975A-1 Sequence 1, Application US/08123975A

Initial Score    =     33  Optimized Score  =     462 Significance =  0.58
Residue Identity =    41%  Matches          =     560 Mismatches   =   711
Gaps             =     91  Conservative Substitutions            =     0

            X       10        20        30        40        50        60
            GAATTCTTAGTTTTCCTGCCAACCGTGTTCTTTAGAGATGAAAGACCAGAAGCAACCGTTAGAAGA
              ||   | || | |   | | |     |   || |     || | ||  |  | |        ||
      CTCGAGCCATGGCTCGTCTGCTGTCTACCTTCACTGAATACATCAAGAACATCATCAATACCTCCATCCTGA
            X 10        20        30        40        50        60        70

        70        80        90        100       110       120       130
      AGTGTTTTTACGGATGTTGTTGTAGTACCATGAAGAAGCAACCAGGTTGTTAGAGTGGAAACCCAGCA----
      |       |||| |      |  | |  | |||   | |   |  |   |  |  |  |||  || ||
      ACCTGCGCTACGAA------TCCAATCACCTGATCGACCTGTCTCG--CTACGCTTCCAAAATCAACATCGG
            80              90        100       110         120       130

         140       150       160       170       180       190       200
      GACCGATGTTACCACCGTTGTTGTTCTGGAAGTTCATAGTGCAGTTGTTACCGATCGAGTCCATAACGAT-G
        |  | |||| |  || |   | ||   |||       | ||| ||||     | || ||    |  || |
      TTCTAAAGTTAACTTCGAT-CCGATCGACAAGAATCAGATCCAGCTGTTCAATCTGGAATCTTCCAAAATCG
       140       150        160       170       180       190       200

        210       220       230       240       250       260       270
      ATCTGACCCAGAGAGTTGTTAGAGTTAGAAGTACGGATCAGTTTGATGATTTTTTCCGGTTTAGCGATAGAG
      |  | | || ||    || ||  ||   |   |    |  ||  ||  | || | |   |    |   |
      AAGTTATCCTGAAGAATGCTATCGT---ATACAACTCTATGTACGAAAACTTCTCCACCTCCTTCTGGA---
      210       220       230          240       250       260       270

      280       290       300       310       320       330       340
      ATGTCAGCGTACAGACGGTATTCAACGTCACGGTCAACAACGTTGATGTAAGCCAGGTCGTTTTTACGTACG
         || |  | | ||     ||||||  ||        |||  |||    | |    ||   |  | | |
      ---TCCGTATCCCGAAATACTTCAACTCCATCTCTCTGAACAATGAATACACCATCATCAACTGCATGGAAA
             280       290       300       310       320       330       340

    350        360       370       380       390       400          410
      A-AGTTGTCAGTGTTAGAGATGTCAGTAGAACCGTTTTTACGGATGATAACTTCAACAC---CAGTGTACAG
      | | || |   ||  |   || || | |  || ||     |   ||    || ||  ||   |||   |
      ACAATTCTGGTTGGAAAGTATCTCTGAACTACGGTGAAATCATCTGGACTCTGCAGGACACTCAGGAAATCA
           350       360       370       380       390       400       410

      420       430       440       450        460        470       480
      ACGAGTGTTAGAGAAGATATTAGGTTTCTGATAAACACCA-CGCTG-CTGGTTGATGTTCAGGAAGTTAGAG
      |  || ||     |    | ||  | || ||| | || || | ||| ||   | |    | |||  || |
      AACAGCGTGTTGTATTCAAATA-CTCTCAGATGATCAACATCTCTGACTACATCAATCGCTGGATCTTCGTT
         420       430        440       450       460       470       480

      490       500       510       520       530       540           550
      TTCTGAGTGATAGATTTGTCAGTCCGGAGCAGGTTCAGCAGGTAGTAACGTTTGTTGTAC----AGCAGGTA
        |      |   ||              ||   ||  ||   |    ||| || |  ||    | | | |
      ACCATCACCAACAATCGTCTGAATAACTCCAAAATCTACATCAACGGCCGTCTGATCGACCAGAAACCGATC
        490       500       510       520       530       540       550

        560       570       580       590       600       610       620
      GTTACCCCAGAAGTCTTTCAGGATAGACGGGTCCGGTTCGTCAGAGTACAGAGTTTCGATTTCAGTTTTACC
         |  |  |    | | || | |        |    |  ||| | |  |  |||    |  || |     |
      TCCAATCTGGGTAACATCCACGCTTCTAATAACATCATGTTCAAACTGGACGGTTGTCGTGACACTCACCGC
      560       570       580       590       600       610       620

      630       640       650       660       670       680       690
      CAGTTCAGTGTCGAAAACTTTGAAGTAACGGATACCAACGTAACGCGTGTCGTTGCAACCAACGATTT----
       |  || |  || || ||||  |  |    ||   ||| | |  |   |     | || ||| ||  |
      TACATCTGGATCAAATACTTCAATCTGTTCGA---CAAAGAACTGAACGAAAAAGAAATCAAAGACCTGTAC
    630       640       650       660          670       680       690

          700       710       720       730       740       750       760
      --TGAACAGGATGTTGTCAGAAACGTGGATGTCACCCAGGTTAGAGATAGATTTTTCATCGATCAGGTTACC
          | |||     |    | | | || | | |  |  || |    |       | |  | | | |     |
      GACAACCAGTCCAATTCTGGTATCCTGAAAGACTTCTGGGGTGACTACCTGCAGTACGACAAACCGTACTAC
     700       710       720       730       740       750       760       770

        770       780       790       800       810         820       830
      GTTGATGTAGATACGAGAGTTACCCAGACGGTTGTTAGTGATAGTAACGAAG--ATCCATTTATTAATGTAG
       |     |  ||  |   | | |  | |     |||   |  |  || | ||  ||||     |  |||||
      AT---GCTGAATCTGTACGATCCGAACAAATACGTTGACGTCAACAATGTAGGTATCCGCGGTTACATGTA-
                780       790       800       810       820       830

        840       850       860         870       880       890       900
      TCAGAGATAGAGATCATCTGAGTGTAGT--TGAAAACCAGTTTCTGGTTGTTACCAGCAGTGTCCTGCAGAG
              | || ||  |   ||   ||  |||  ||||   |||   ||    |  |  ||| | |  |
      ----CCTGAAAGGTCCGCGTGGTTCTGTTATGACTACCAACATCTACCTGAACTCTTCCCTGTACCGTGGTA
         840       850       860       870       880       890       900
      910       920       930      940       950       960       970
    TCCAGATGATTTTGTTGTAGTTCAGAGAGATTTCCAACCAGAGTTGTTGTTACGGATGCAGTCGATGATAG
     | |  | ||  |   | |    | |    | |  ||| ||    |    ||  | |     | ||||| |
    CCAAATTCATCATCAAGAA----ATACGCGTCTGGTAACAAG----GACAATATCGTTCGCAACAATGATCG
     910       920          930       940           950       960      970

    980          990     1000      1010      1020           1030      1040
    TGTAT---TCGTTGTTCAGGTTAACTTTGTTGAAGTATTTCGGGATACGAA-----CCCAGAAAGAGATAGA
    |||||   ||  ||||   |||||       |||     || || ||| ||    | |||   |   ||||
    TGTATACATCAATGTTGTAGTTAAGAACAAAGAATACCGTCTGGCTACCAATGCTTCTCAGGCTGGTGTAGA
           980       990     1000      1010      1020      1030      1040

         1050       1060     1070      1080      1090      1100      1110
    GAAGTTCTGGT-AACGACCGTTGTAGATGATGTCGTTGTTCTGAGCGATGTTTACTTCAGACGGTTTAGAAG
     ||| ||| ||   |    |   |    || || | |  ||||   | |  || ||   | |   |  |||
    AAAGATCTTGTCTGCTCTGGAAATCCCGGACGTTGGTAATCTGTCTCAGG--TAGTTGTAATGAAATCCAAG
        1050      1060      1070     1080      1090        1100      1110

        1120      1130     1140      1150      1160      1170      1180
    AGTAGATACCGAACTGGTTGCGGTTAGTAGAGTAGATGTAGACGTCACCGTTGATAGAGATGTTAGAACCAT
    |      |  | |    |  |   | | | | | || |  | | || |  || ||  ||| |  |   |||
    AACGACCAGGGTATCACTAACAAAT-GCAAAATGAATCTGCAGGACAACAATGGTAACGATATCGGTTTCAT
        1120      1130      1140      1150      1160      1170      1180

                  1190     1200      1210        1220      1230      1240
    AG------------CCAGAGATGTCGATGAATTTGTTGTTTTC--GTAACGCATGTCCAGGATAGAGTTGTC
     |             ||   || ||| | || | |||| ||  |  |    ||       ||| ||    ||
    CGGTTTCCACCAGTTCAACAATATCGCTAAACTGGTTGCTTCCAACTGGTACAATCGTCAGATCGAACGTTC
       1190      1200      1210      1220      1230      1240      1250

        1250      1260     1270      1280      1290      1300      1310  X
    TTTGATTTTTTTGTACAGTTTGTTGAAGTACAGGATCAGGATTTTGTCGTTAGTGTAAGACATCGTGAATTC
     |       | ||    | |  | | ||| ||   | || |  || || | | |    || ||     |
    CTCTCGCACTCTGGGTTGCTCTTGGGAGTTCA--TCCCGGTTGATGACGGTTGGGGTGAACGTCCGCTGTAA
     1260      1270      1280       1290      1300      1310      1320   X

    CCCGGGAAAGCTT
     1330

3. US-09-910-186A-33’ (1-1314)
   US-08-123-975A-6 Sequence 6, Application US/08123975A

Initial Score     =     27  Optimized Score   =    458  Significance = -1.15
Residue Identity  =    40%  Matches           =    553  Mismatches   =   727
Gaps              =    102  Conservative Substitutions             =     0

     X      10        20       30        40        50        60       70
    GAATTCTTAGTTTTCCTGCCAACCGTGTTCTTTAGAGATGAAAGACCAGAAGCAACCGTTAGAAGAAGTGTT
     |   |||        | | |  |       |  | |  |    || ||| |  |  |   ||||
     ATGGCTTTCAACAAATACAATTCCGAAATCCTGAACAATATCATCCTGAACCTGCGTTACAAAGACAACAA
     X       10        20        30        40        50        60        70

          80        90       100              110       120       130
    TTTACGGATGTTGTTGTAGTACCATGAAGAAG-------CAACCAGGTTGTTAGAGTGGAAACCCAGCAGAC
    | |        |||     |||  ||   |||        || | | ||||  | || |   | || |
    TCTGATCGATCTGTCTGGTTACGGTGCTAAAGTTGAAGTATACGACGGTGTTGAACTGAATGACAAGAA---
           80        90       100       110       120       130       140

    140       150       160       170      180       190       200
    CGATGTTACCACCGTTGTTGTTCTGGAAGTTCATAGTGCAGTTGTTACCGATCGAGTCCATAACGATGATCT
        |||   || |   |  | |   || |  |  | |   |    | ||   ||  ||| |   | | ||
    -CCAGTTCAAACTGACCTCTTCCGCTAACTCTAAGATCCGTGTTACTCAGAATCAGAACATCATCTTCAACT
            150       160       170       180      190       200       210

  210       220       230       240       250            260       270
    GACCCAGAGAGTTGTTAGAGTTAGAAGTACGGATCAGTTTGATGATTT------TTTCCGGTTTAGCGATAG
              |   ||     |     |  ||||| || |   ||  |         |||| |   ||
    CCGTATTCCTGGACTTCTCTGTTTCCTTCTGGATCCGTATCCCGAAATACAAGAACGACGGTATCCAGAATT
          220       230       240       250       260       270      280

       280       290       300       310           320       330       340
    AGAT-GTCAGCGTACAGACGGTATTCAACGTCACGGTCAACAAC-----GTTGATGTAAGCCAGGTCGTTTT
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  | ||   ||  | | | ||  |  |||||  || |   || |||      | || |    |||       |
  ACATCCACAATGAATACACCATCATCAACTGCATGAAGAATAACTCTGGTTGGAAGATCTCCATCCGCGGTA
      290       300       310       320       330       340       350

        350       360        370       380       390       400       410
  TACGTACGAAGTTGTCAGTGTTAGAGAT-GTCAGTAGAACCGTTTTTACGGATGATAACTTCAACACCAGTG
    ||||  |  | | |  || | || ||   | |||  |||   | |          | | ||||| | |||
  ACCGTATCATCTGGACTCTGATCGATATCAACGGTAAGACCAAATCTGTATTCTTCGAATACAACATCCGTG
    360       370       380       390       400       410       420

       420       430       440          450       460       470       480
  TACAGACGAGTGTTAGAGAAGATATTAGG---TTTCTGATAAACACCACGCTGCTGGTTGATGTTCAGGAAG
   | | |    ||         ||    ||   ||  | |  | |||||     |||    ||| | |  ||
  AAGACATCTCTGAATACATCAATCGCTGGTTCTTCGTTACCATCACCAATAACCTGAACAATGCTAA--AAT
  430       440       450       460       470       480       490

        490       500       510        520        530       540       550
  TTAGAGTTCTGAGTGATAGATTTGTCAGTCCG-GAGCAGGTTCAGCAG-GTAGTAACGTTTGTTGTACAGCA
   || |     |    |  |   | | |  |||  | ||    || | | | ||| |    |   |   |
  CTACATCAACGGTAAACTGGAATCTAATACCGACATCAAAGACATCCGTGAAGTTATCGCTAACGGTGAAAT
  500       510       520       530       540       550       560

        560       570       580       590       600       610       620
  GGTAGTTACCCCAGAAGTCTTTCAGGATAGACGGGTCCGGTTCGTCAGAGTACAGAGTTTCGATTTCAGTTT
    |  | |  |  || |        |||   ||   || |||| || |  |  |    |||    ||
  CATCTTCAAACTGGACGGTGACATCGAT---CGTACCCAGTTCATCTGGATGAAATACTTCTCCATCTTCAA
570       580       590          600       610       620       630

      630       640       650            660       670       680       690
  TACCCAGTTCAGTGTCGAAAACTTTGAA-----GTAACGGATACCAACGTAACGCGTGTCGTTGCAACCAAC
   ||| |  |   |      ||  | |||     |||   ||| |   | ||   ||  |   || ||
  CACCGAACTGTCTCAGTCCAATATCGAAGAACGGTACAAGATCCAGTCTTACTCCGAATACCTGAAAGACTT
 640       650       660       670       680       690       700       710

         700       710             720        730       740       750
  GATTTTGAACAGGATGTTGT------CAGAAACGTGGATG-TCACCCAGGTTAGAGATAGATTTTTCATCGA
         ||   | || |||       ||||   |  ||| |||     | ||   | |  | || |||| |
  CTGGGGTAATCCGCTGATGTACAACAAAGAATACTATATGTTCAATGCTGGTAACAAGAACTCTTACATCAA
         720       730       740       750       760       770       780

    760       770       780       790       800       810       820
  TCAGGTTACCGTTGATGTAGATACGAGAGTTACCCAGACGGTTGTTAGTGATAGTAACGAAGATCCATTTAT
   | |   |  |    |   | |    | |  | || |||  | |||    |||  | |  ||| |  |  ||
  ACTGAAGAAAGACTCTCCGGTT---GGTGAAATCCTGAC--TCGTTCCAAATACAACC--AGAACTCTAAAT
       790       800          810         820       830         840

  830       840       850       860       870       880       890
  TAATGTAGTCAGAGATAGAGATCATCTGAGTGTAGTTGAAAACCAGTTTCTGGTTGTTACCAGCAGTGTCCT
    ||  | |          |  |||| | |   |||| |  | | ||             |   | | |
  ACATCAACTACCGCGACCTGTACATCGGTGAAAAGTTCATCATCCGT-------------CGCAAATCTAAC
  850       860       870       880       890                    900

900         910       920       930         940       950       960
  GCAGAGTCCA--GATGATTTTGTTGTAGTTCAGAGAGATT--TTCCAACCAGAGTTGTTGTTACGGATGCAG
   |  ||||||   |||||    | |||  | |   ||| |   || | |  || || ||    | ||  |||
  TCTCAGTCCATCAATGATGACATCGTACGTAAAGAAGACTACATCTACCTGGACTTCTTCAACCTGAATCAG
   910       920       930       940       950       960       970

  970       980             990       1000      1010      1020      1030
  TCGATGATAGTGTATTC------GTTGTTCAGGTTA-ACTTTGTTGAAGTATTTCGGGATACGAACCCAGAA
       |   || ||  |      ||  |||| |  | |    |   |  | || | || | ||| | | ||
  GAATGGCGTGTATACACCTACAAGTACTTCAAGAAAGAAGAAGAAAAGCTTTTCCTGGCTCCGATCTCTGAT
 980       990      1000      1010      1020      1030      1040      1050

      1040      1050      1060      1070      1080      1090      1100
  AGAGATAGAGAAGTTCTGGTAACGACCGTTGTAGATGATGTCGTTGTTCTGAGCGATGTTTACTTCAGACGG
     ||    |            |      |   |||  | | ||     | || | |   || |      | |
  TCCGACGAACTCTACAACACCATCCAGATCAAAGAATACGACGAACAGCCGACCTACTCTTGCCAGCTGCTG
        1060      1070      1080      1090      1100      1110      1120

    1110               1120      1130      1140      1150      1160
  TTTAGAAGAGTAGA---------TACCGAACTGGTTGCGGTTAGTAGAGTAGATGTAGACGTCACCGTTGAT
  || |  | ||  ||         |  |||| | | |  | |  |||       | |  |||   | | | ||
  TTCAAGAAAGATGAAGAATCTACTGACGAAATCGGTCTGATCGGTATCCACCGTTTCTACGAATCTGGT-AT
      1130      1140      1150      1160      1170      1180      1190

 1170      1180      1190      1200               1210      1220
  AGAGATGTTAGAACCATAGCCAGAGATGTCGAT---------GAATTTGTTGTTTTCGTAACGCA---TGTC
   |   |   ||||    |     |  | |  ||         | |  ||  |       ||||||    ||
  CGTATTCGAAGAATACAAAGACTACTTCTGCATCTCCAAATGGTACCTGAAGGAAGTTAAACGCAAACCGTA
     1200      1210      1220      1230      1240      1250      1260

 1230      1240      1250      1260      1270      1280      1290
  CAGGATAGAGTTGTCTTTGATTTTTTTGTACAGTTTGTTGAAGTACAGGATCAGGATTTTGTCGTTAGTGTA
  ||   |  |  ||  ||  | ||    || ||   |   |||  ||       |||     | || |
  CAACCTGAAACTGGGTTGCAATTGGCAGTTCA---TCCCGAAAGACGAAGGTTGGACCGAATAGTAACCTCT
   1270      1280      1290         1300      1310      1320      1330

1300     1310   X
  AGACATCGTGAATTC
  |||      |  | |
  AGAGTCGAGGCCTGCAG
    1340      1350
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-910-186a-34.res made by bobryen on Thu 7 Nov 102 14:38:25-PST.


Query sequence being compared:US-09-910-186A-34 (1-432)
Number of sequences searched:                         3
Number of scores above cutoff:                        3

       Results of the initial Comparison of US-09-910-186A-34 (1-432) with:
         File : US08123975A.pep
   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-
Q     -
U     -
E     -
N     -
C     -
E     -                                                 * *          *
S    0---------------------------------------------------------------------
      ||     | |    | |    | |    |  |   |  |   |  |   |   |  |   |  |
SCORE 0|    23 |   46 |   69 |   92  | 116  | 139  | 162   |185   |208
STDEV -7      -6     -5     -4      -3     -2     -1       0      1

                                PARAMETERS

Similarity matrix         PAM-150     K-tuple                          1
Threshold level of sim.       16%
Mismatch penalty                1     Joining penalty                 20
Gap penalty                  5.00     Window size                    432
Gap size penalty             0.05
Cutoff score                    1
Randomization group             0

                                SEARCH STATISTICS

Scores:                    Mean        Median      Standard Deviation
                            181          165          23.64

Times:                     CPU                      Total Elapsed
                       00:00:00.00                  00:00:00.00

Number of residues:                      1704
Number of sequences searched:               3
Number of scores above cutoff:              3


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                        Init. Opt.
Sequence Name      Description                   Length Score Score  Sig. Frame
-------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
   1. US-08-123-975A-2 Sequence 2, Application U    850   208   264   1.14   0
                    ****  0 standard deviation from mean ****
   2. US-08-123-975A-3 Sequence 3, Application U    415   171   296  -0.42   0
   3. US-08-123-975A-5 Sequence 5, Application U    439   164   256  -0.72   0


1. US-09-910-186A-34 (1-432)
   US-08-123-975A-2 Sequence 2, Application US/08123975A

Initial Score    =    208  Optimized Score  =    264  Significance =  1.14
Residue Identity =    35%  Matches          =    163  Mismatches   =   231
Gaps             =     28  Conservative Substitutions              =    33

                        X       10        20        30        40        50
                        MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVY
                          |||| |||  |||    |  | || :||  |  || ||||: : :   |
    AEYEKSKVNKYLKTIMPFDLSIYTNDTILIEMFNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVE
  380       390       400       410       420       430       440       450

          60        70        80        90       100          110       120
    IYSTNRNQFGIYSSKPSEVNIAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRNNNSG
         :|||   ||  | : : ||  ||:|  :  ||:|||:||||| |        |||||| | : ||||
    L--NDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSG
            460       470       480       490       500       510        520

          130       140       150       160       170       180       190
    WKISLNYNKIIWTLQDTAGNNQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLG
    ||||   |:||||| |  |      | |     ||:|||:| ||||||| | |::||||| |     |
    WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIR
           530       540       550       560        570       580       590

        200       210        220       230       240       250       260
    DIHVSDNILFKIVGCND-TRYVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLL
    ::     | ||  |  | | ::  :|| :| |||    ||  |        ||||||| |:||| ||: |
    EVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAG
          600       610       620       630       640       650       660

       270        280       290       300       310       320       330
    RTDKSITQNSNF-LNINQQRGVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDV
         |             |  |     : | |     |  | :  |   |  |  ||| |  |
    NKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQ
        670       680       690       700       710       720       730

      340       350       360       370            380       390
    EYRLYADISIAKPEKIIKLIRTSNSNNSLGQIIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH-------
    | | |      | |    |   | |      | : :                      ||| | |
    EWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGI
      740       750       760       770       780       790       800

           400       410         420          X
    -----SNNLVASSWYYNNIRKN--TSSNGCFWSFISKEHGWQEN
               | ||   :::       || | || |: || |
    VFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE
    810       820       830       840       850


2. US-09-910-186A-34 (1-432)
   US-08-123-975A-3 Sequence 3, Application US/08123975A

Initial Score    =    171  Optimized Score  =    296  Significance = -0.42
Residue Identity =    49%  Matches          =    205  Mismatches   =   168
Gaps             =     17  Conservative Substitutions              =    27

    10        20        30        40        50        60        70        80
    LILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVNIAQNNDII
                        ||| |  || | |:| | |   |      :||   :    | : :   | |:
                        RYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
                        X       10        20        30        40        50
         90       100       110       120       130       140       150
 YNGRYQNFSISFWVRIPKYFNKVNLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGNNQKLVFNYTQM
 ||  | ||| |||:||||||| : |||||||| |   ||||||:||||  ||||||||    |: || | ||
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQM
       60        70        80         90       100       110       120

      160       170       180       190       200       210        220
 ISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCNDT-RYVGIRYFKVFD
 | ||||||:||||||||||| ||:||||| ||| | ||||| || | ||:||  || || ||: |:||  ||
 INISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFD
     130       140       150       160       170       180       190

     230       240       250       260       270           280       290
 TELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNS----NFLNINQQRGVYQKPNI
  ||   ||  ||       ||||||| || | | ||:|||    | :  |      ::     ||     ||
 KELNEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNI
   200       210       220       230       240       250       260

       300       310       320       330       340       350       360
 FSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLIRTSNSNNS
 : |  || |   ||:| :|    | || || ||  ||||| :  ||||    | |  |||          |
 YLNSSLYRGTKFIIKKYAS---GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNL
 270       280          290       300       310       320       330

     370           380       390           400       410       420
 LGQIIVM----DSIGNNCTMNFQNNNGGNIGLLGFHS----NNLVASSWYYNNIRKNTSSNGCFWSFISKEH
    ::        | | | || | |||  ||  |||       |||| ||   | :     || | ||  :
 SQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDD
  340       350       360       370       380       390       400

 430 X
 GWQEN
 || |
 GWGERPL
410  X


3. US-09-910-186A-34 (1-432)
   US-08-123-975A-5 Sequence 5, Application US/08123975A

Initial Score    =    164  Optimized Score  =    256  Significance = -0.72
Residue Identity =    35%  Matches          =    156  Mismatches   =   226
Gaps             =     28  Conservative Substitutions           =    33

          10  X     20        30        40        50        60        70
  MSYTNDKILILYFNKLYKKIKDNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVN
              |||    |  | || :||  |  || ||||: : :   |      :|||   ||  | :
              FNKYNSEILNNIILNLRYKDNNLIDLSGYGAKVEVYDGVEL--NDKNQFKLTSSANSKIR
              X       10        20        30        40          50

        80        90       100          110       120       130       140
  IAQNNDIIYNGRYQNFSISFWVRIPKYFNKV---NLNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGN
  : ||  ||:|  :  ||:|||:||||| |        |||||| | : ||||||||   |:||||| |  |
  VTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMK-NNSGWKISIRGNRIIWTLIDINGK
  60        70        80        90       100        110       120

        150       160       170       180       190       200       210
  NQKLVFNYTQMISISDYINKWIFVTITNNRLGNSRIYINGNLIDEKSISNLGDIHVSDNILFKIVGCND-TR
       | |     ||:|||:| ||||||| | |::||||| |     |    ::    .| ||  |  | |
  TKSVFFEYNIREDISEYINRWFFVTITNN-LNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQ
130       140       150        160       170       180       190       200

       220       230       240       250       260       270        280
  YVGIRYFKVFDTELGKTEIETLYSDEPDPSILKDFWGNYLLYNKRYYLLNLLRTDKSITQNSNF-LNINQQR
  ::  :|| :| |||    ||  |        ||||||| |:||| ||: |       |             |
  FIWMKYFSIFNTELSQSNIEERYKIQSYSEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTR
         210       220       230       240       250       260       270

      290       300       310       320       330       340       350
  GVYQKPNIFSNTRLYTGVEVIIRKNGSTDISNTDNFVRKNDLAYINVVDRDVEYRLYADISIAKPEKIIKLI
    |     : | |     |  | :  |   |  |  ||| |  |        | | |      | |    |
  SKYNQNSKYINYRDLYIGEKFIERRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLA
       280       290       300       310       320       330       340

    360       370            380       390                   400       410
  RTSNSNNSLGQIIVMD-----SIGNNCTMNFQNNNGGNIGLLGFH------------SNNLVASSWYYNNIR
    | |      | : :                      ||| | |                  | ||   ::
  PISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVK
     350       360       370       380       390       400       410

           420       430
  KN--TSSNGCFWSFISKEHGWQEN
  :       || | || |: || |
  RKPYNLKLGCNWQFIPKDEGWTE
   420       430        X
```